

5914

347  
344  
350

591/e

591/e

591/e



59/1

FIGURE 1D

5'-GGG-3'

1114	CCCCGACCTCCGCCCCAGGACCTGGCCGTTTGGCCCCCTGAGGGAGCCGCTGACCTCTGCCCCGGCCGACG	
1115	C . . . . . A . . . . . AG . . . . . C . . . . . A . . . . . T . G . . . . . CC . . . . . C . . . . .	1114
1116	AA . . . . . G . . . . . G . . . . . C . . . . . C . . . . . G . . . . . T . C . . . . . A . A . . . . .	1115
1117	C . . . . . C . . . . . C . . . . . TC . . . . . G . . . . . A . . . . . G . . . . .	1120
1118	ACCCGATGCTCCCTCCCTACCTCCCTGGACCCCTCCACACACGACCCGCGGCTGGCGGGGGGCTACCG	
1119	. . . . . G . . . . . T . . . . . T . . . . . T . . . . . G . . . . .	1184
1120	. . . . . G . . . . . T . . . . . T . . . . . T . . . . . G . . . . .	1181
1121	. . . . . G . . . . . T . . . . . T . . . . . T . . . . . G . . . . .	1190
1122	CGCGGACTCGACCGGAGGAGCCGCGGCGGAGCGGCGGCTCCCTGCTTCCXGACCTCTTCCXGACCTCTTCCXGAC	
1123	C . . . . . G . . . . . GC . . . . . T . . . . . CCC . . . . . GTC . . . . . G . . . . .	1254
1124	T . . . . . A . . . . . GG . . . . . C . . . . . A . . . . . AAA . . . . .	1251
1125	. . . . . C . . . . . C . . . . . C . . . . . C . . . . . CAT . G . . . . . CCTTA . . . . .	1260
1126	CGCCCTGACCGCGGAGGACGAGCCCTCCCTTGGCTTTACGAGGAGGCTGGAGAGCCGCTTCCCGGCTCCCTCG	
1127	C . . . . . A . . . . . AC . C . . . . . G . . . . . G . . . . . CCT . . . . .	1324
1128	C . . . . . A . . . . . C . . . . . G . . . . . G . . . . . G . . . . . CT . . . . .	1321
1129	C . . . . . A . . . . . C . . . . . C . . . . . A . . . . . C . . . . .	1330
1130	CGCAGATCGACCGCGGCTGCGGCTGGACGCTGGGCTACCTCCAGCCGCTTCCCTGGAGGCTGGCGGA	
1131	GG . . . . . G . . . . . C . . . . . T . . . . . AG . . . . . T . G . . . . . C . . . . .	1394
1132	. . . . . C . . . . . A . . . . . T . . . . . T . . . . . G . . . . . A . . . . . C . . . . .	1391
1133	. . . . . C . . . . . A . . . . . T . . . . . T . . . . . T . . . . . C . . . . . T . . . . .	1400

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FIGURE 1F

[illegible]

FIGURE 1G

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SEQUENCE	ACCTTCCCCAAGGTGCGGGCCCTGCATTGAGAAACACCTGCACGACCCGAGGAGGGGGGTACGTGGAGA	2164
REFSEQ	.....	2161
DIFFER	A.....	2170
SEQUENCE	CCCTCTTCGGCCCCCGCGCGGTACGTGCCCCGACCTCAAGCCCCCGGTGAACAGCGGTGCGGGAGCGGGCGGCA	
REFSEQ	.....	2234
DIFFER	.....	2231
DIFFER	AA.AA.....	2240
SEQUENCE	CCGCATGCGCCCTTCAACATGCCCCGTCCAGGGGCACCGCGCGGACCTCATGAAGCTGCCCATGCGTCAAGCTC	
REFSEQ	.....	2304
DIFFER	.....	2301
DIFFER	.....	2310
SEQUENCE	TCCCCCGCGGTACAGGAAATGCGGGCCCGCAGGATGCTCCITXCAAGTCCACCCAGCAGCTGCTCCAGCGCCC	
REFSEQ	.....	2374
DIFFER	A.....	2371
DIFFER	.....	2380
SEQUENCE	CCGACAGACCGCGCGCGCGGCGGTGCGGGCCCTTGGCCCAAGGAGCTCATGACGGGGGTCTATCGCCCTGCGCCGT	
REFSEQ	.....	2444
DIFFER	A.....	2441
DIFFER	.....	2450

CCCTGGAGGTGGACGTGGGGATGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

## FIGURE 1H

CCCTGGAGGTGGACGTGGGGATGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

CCCTGGAGGTGGACGTGGGGATGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

CCCTGGAGGTGGACGTGGGGATGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

CCCTGGAGGTGGACGTGGGGATGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

2499

2498

2503

591/8



FIGURE 2A

[illegible]

591/01

[illegible]

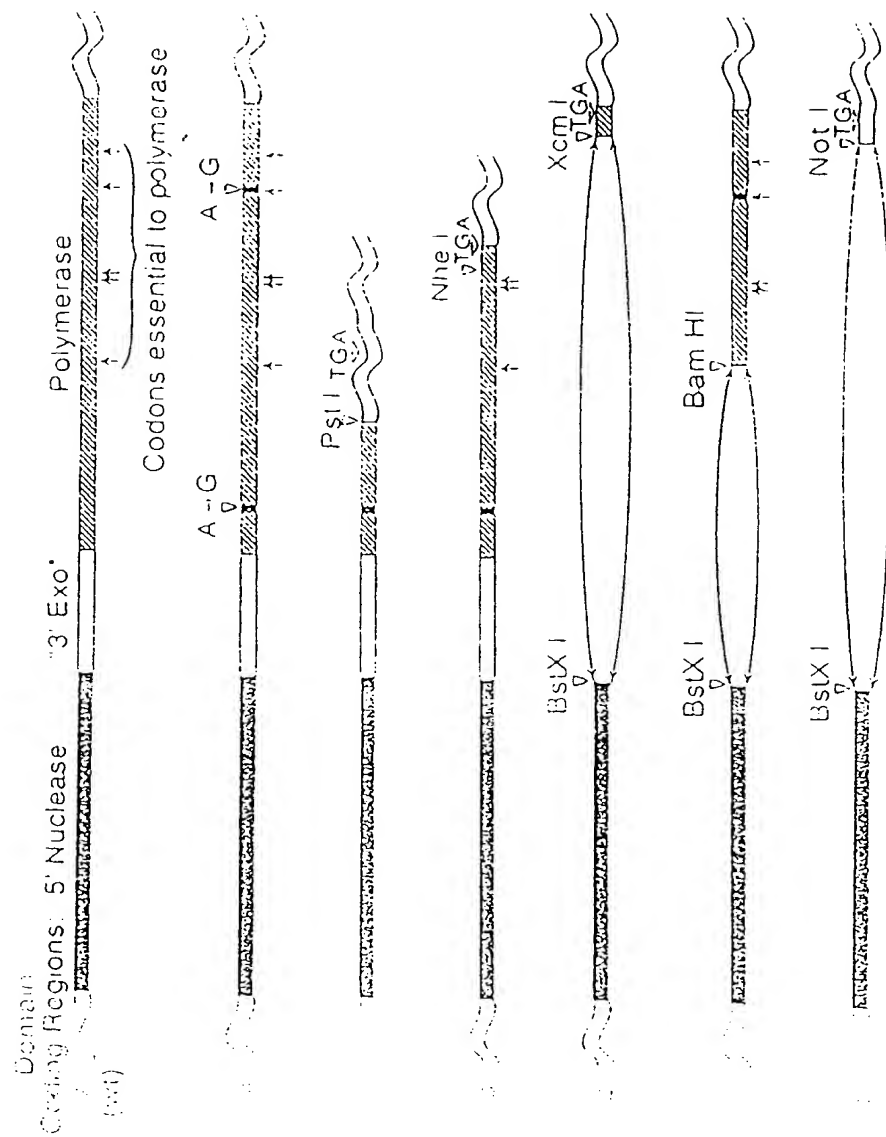
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# FIGURE 2C

SEQUENCE	SFPKURAWI EKILEGRRRCYVETLFCRRRYVPDLNARVKSUREAERMAFHPVQCTAADLHKLAIVXLI	
768	.....E.....	768
769	Y.....G.....	767
770	.....K.....	770
SEQUENCE	EPRLXEMGARMILLOVHDELVLLEAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
833	E.....E...A...R.....	833
834	O...L.....D...R.....W...O.....	831
835	R.....L...OA...E...A...KA.....M.....C	835

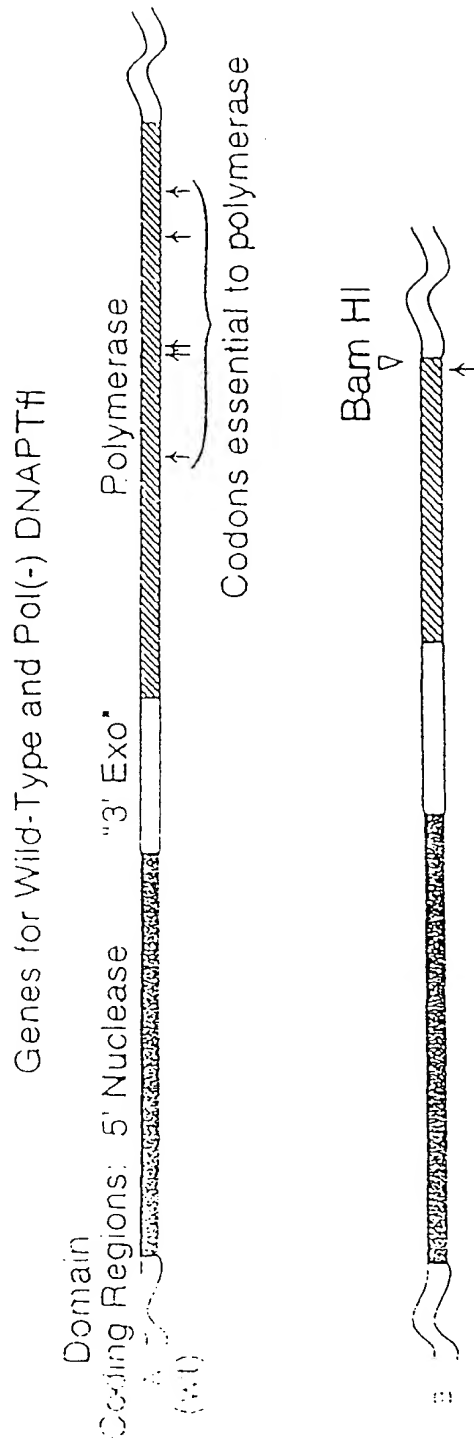
12/1/85

FIGURE 3



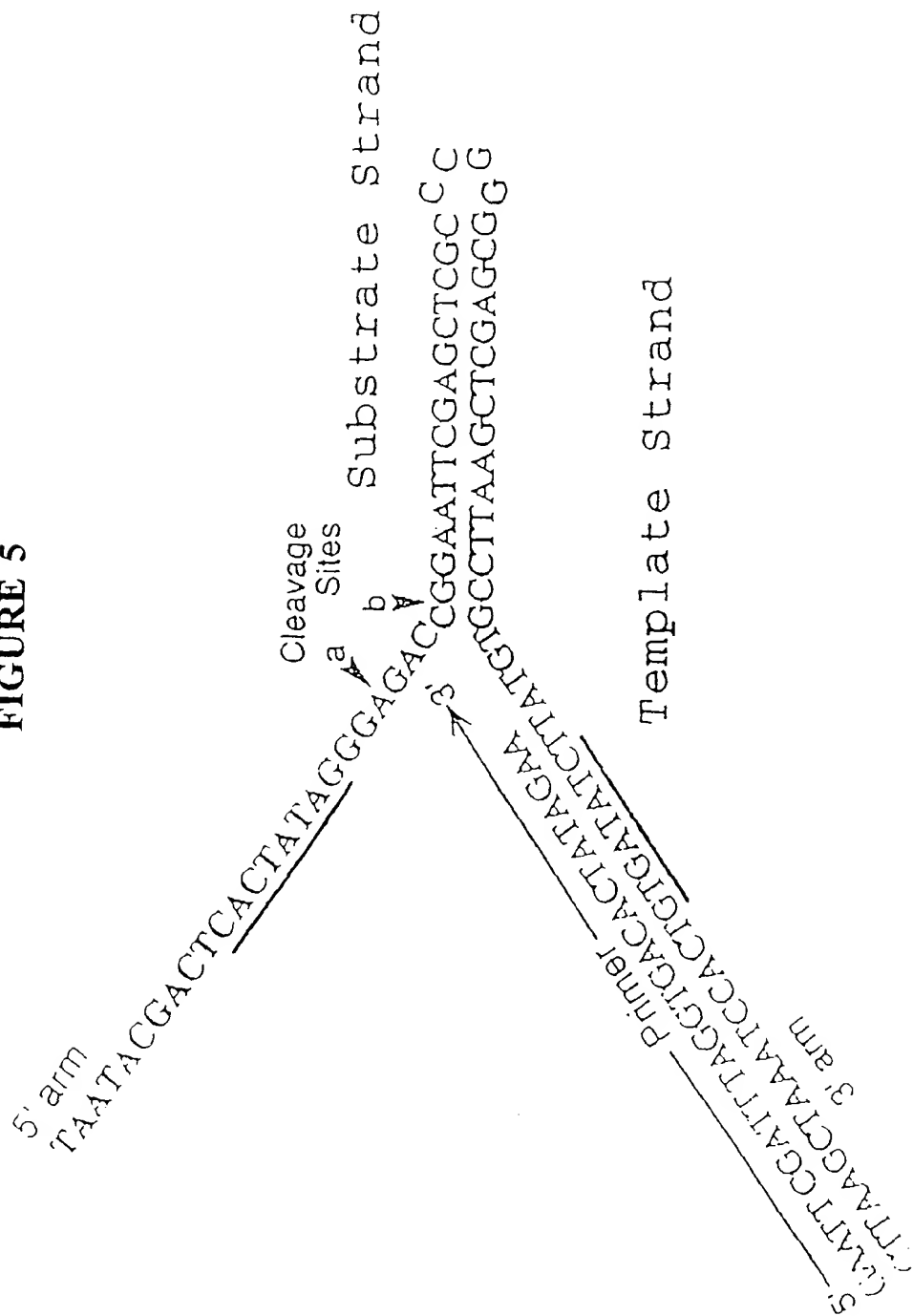
13/16s

FIGURE 4



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FIGURE 5



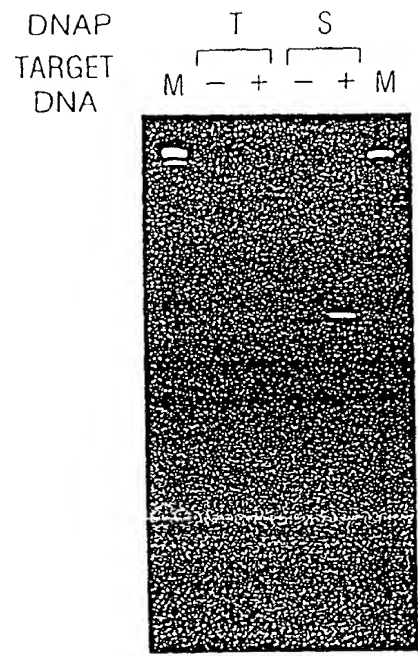


FIGURE 6

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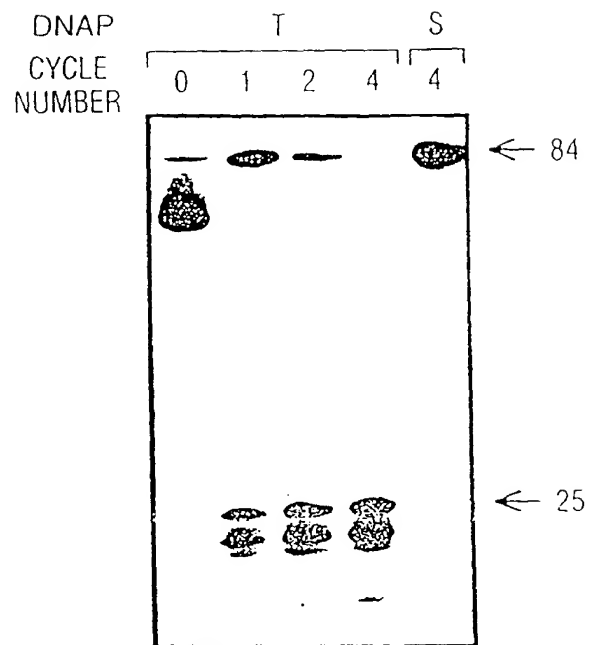


FIGURE 7

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	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

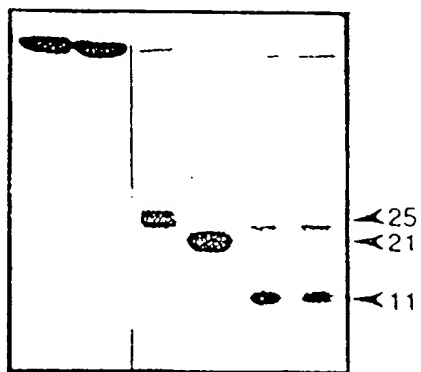


FIGURE 8A

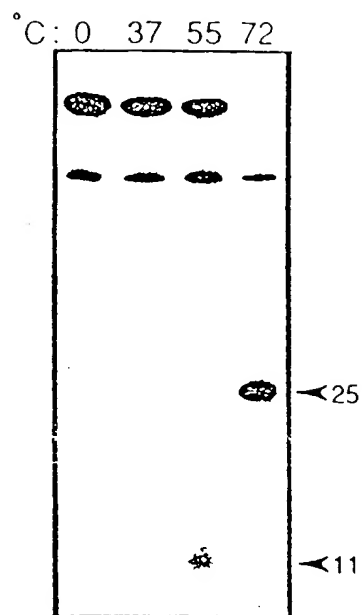


FIGURE 8B

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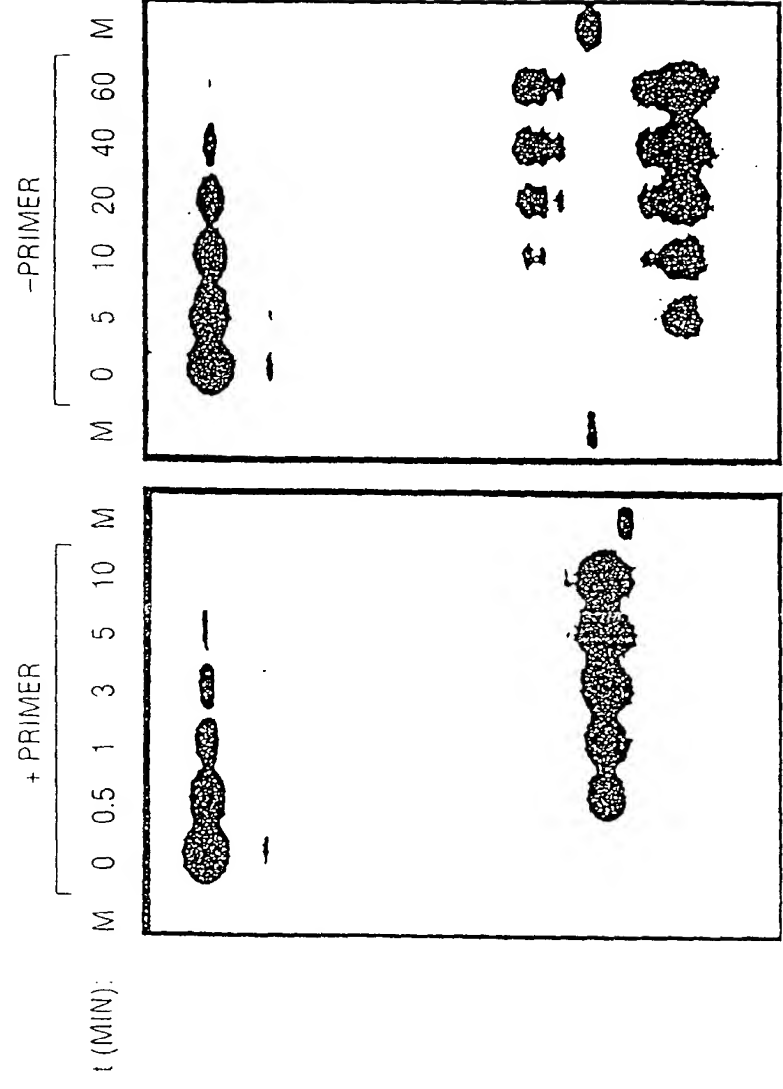
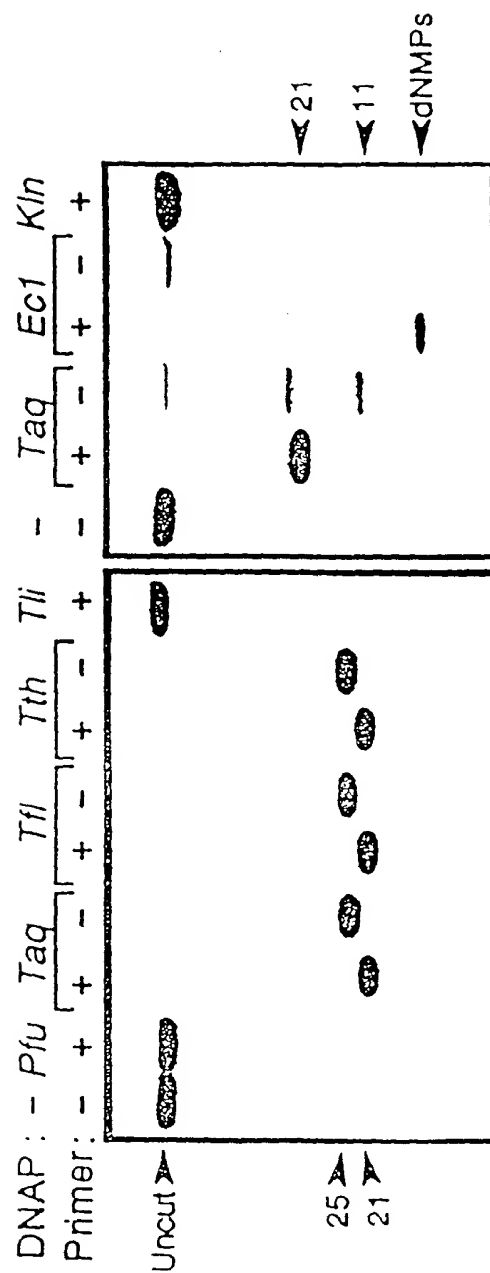


FIGURE 9A

FIGURE 9B

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**FIGURE 10B**

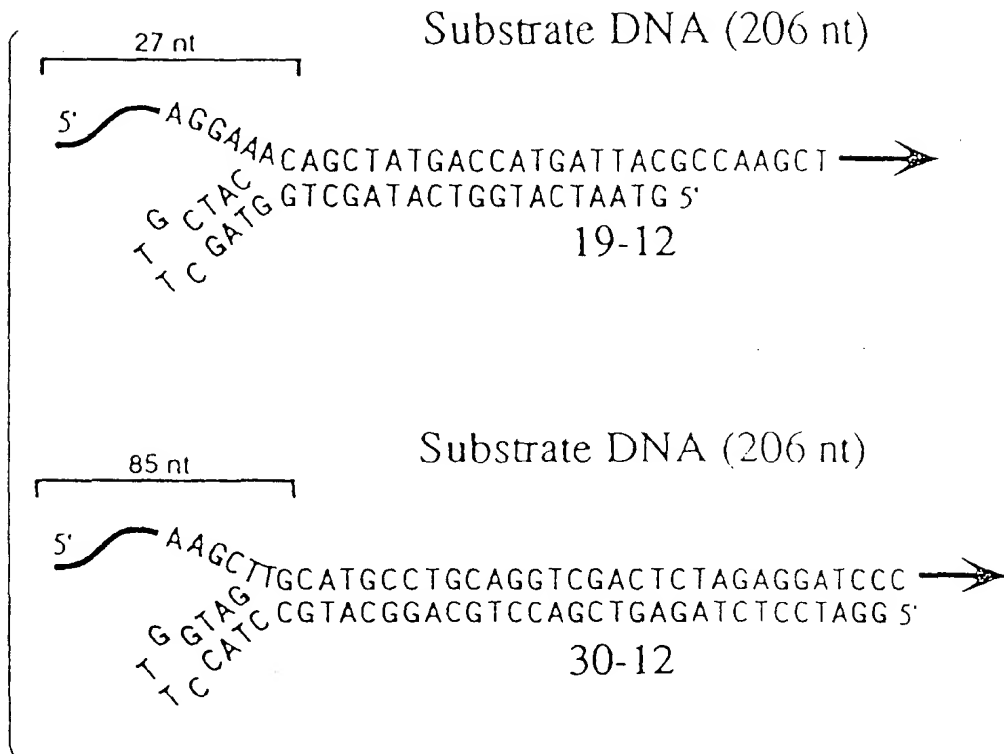


FIGURE 11A

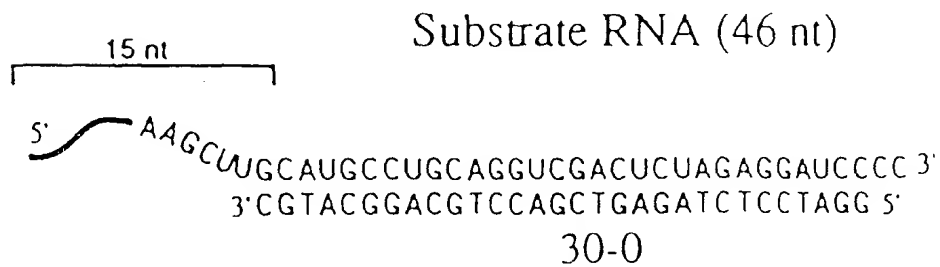


FIGURE 12A

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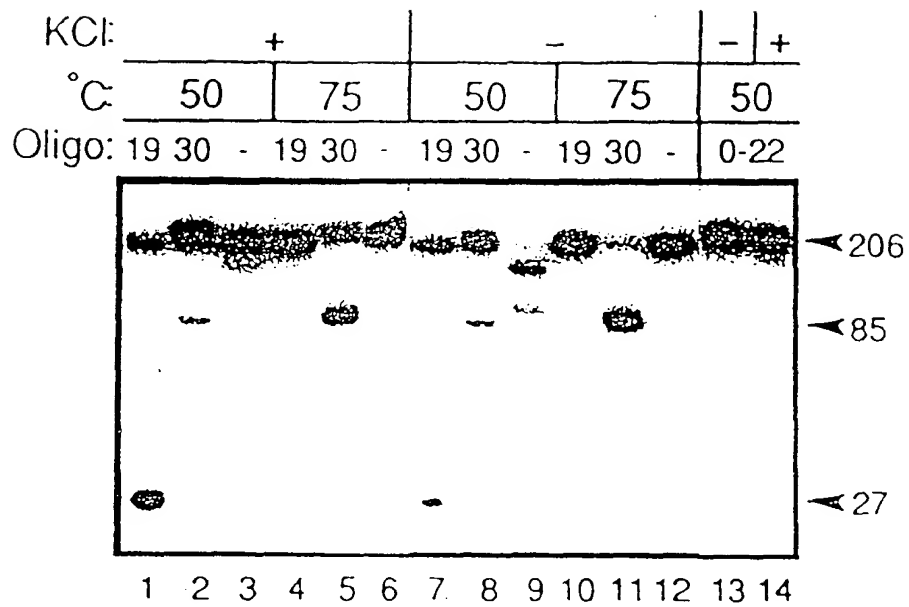


FIGURE 11B

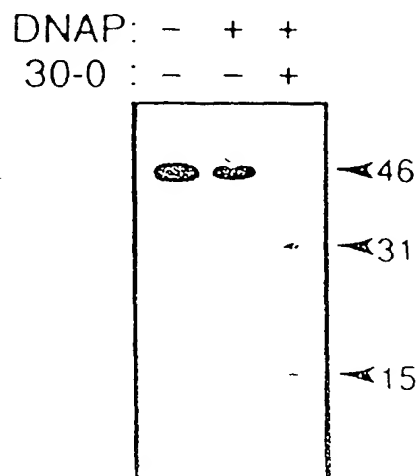


FIGURE 12B

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591/CC

FIGURE 13

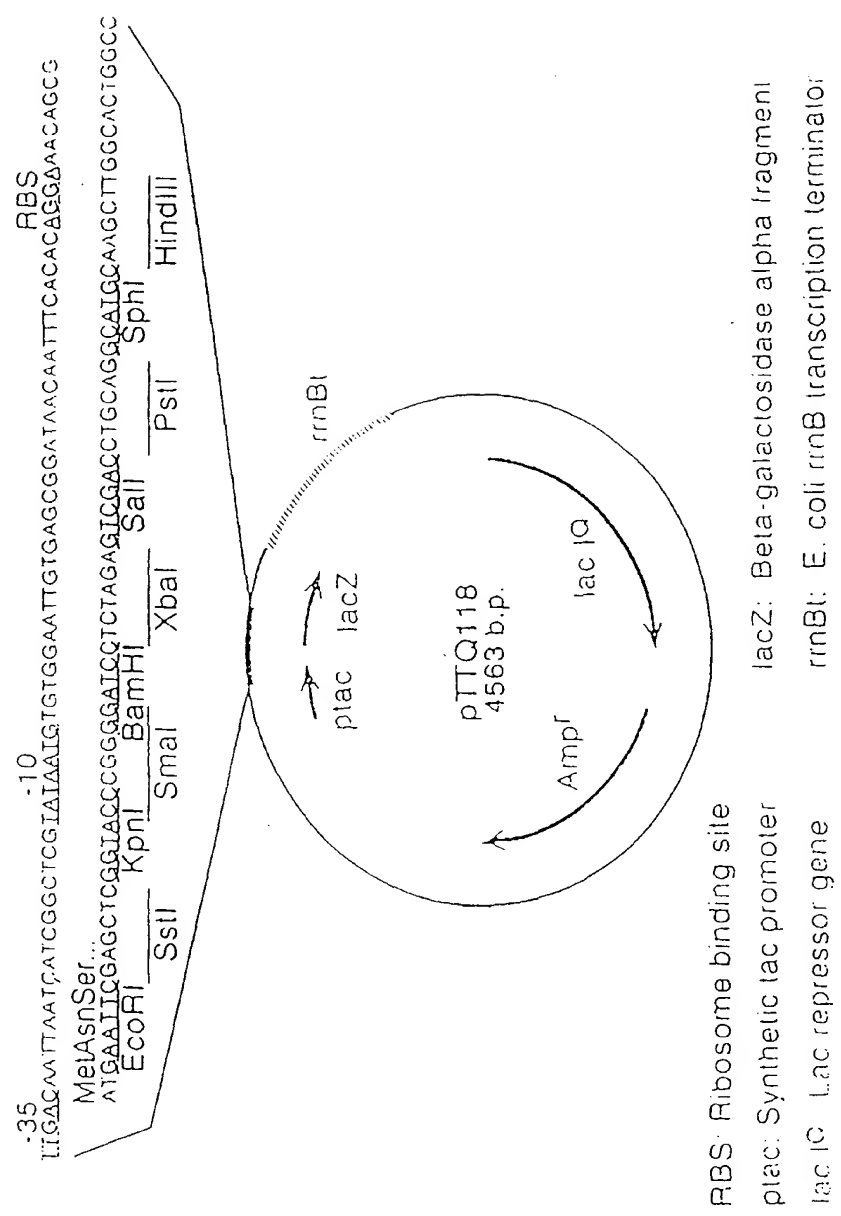
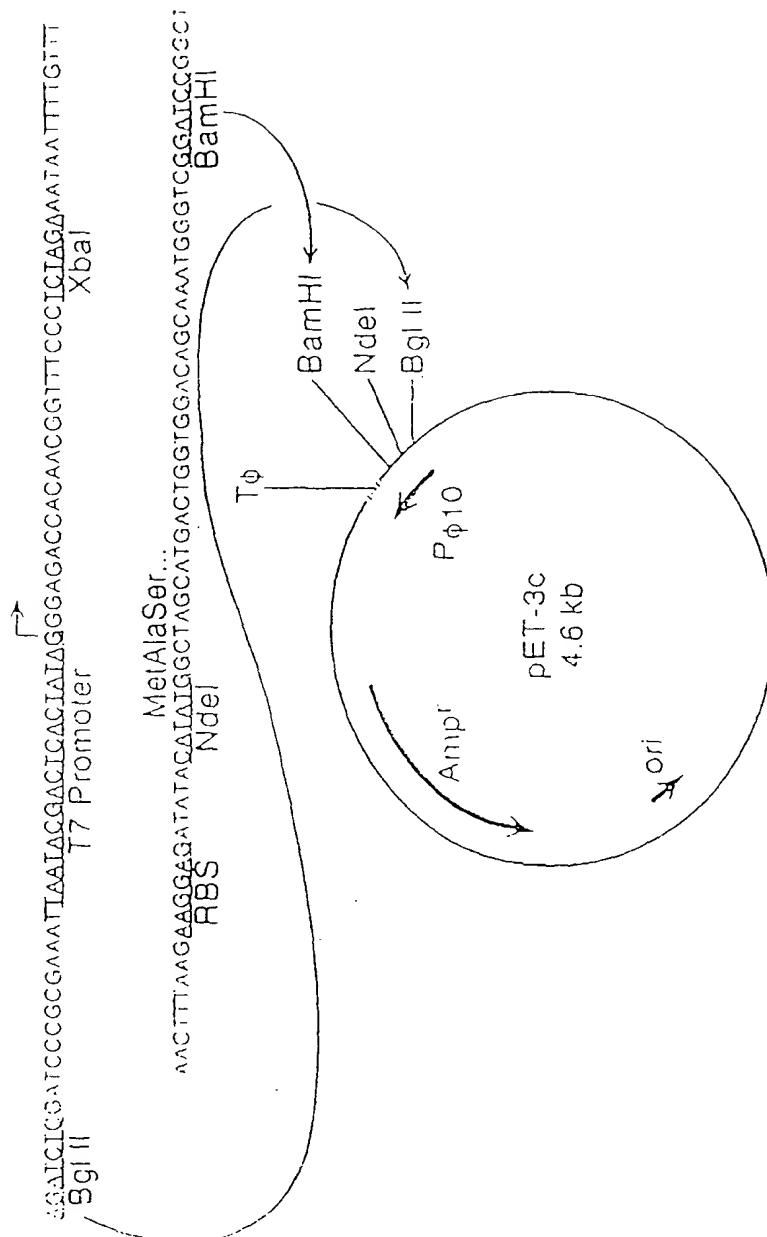


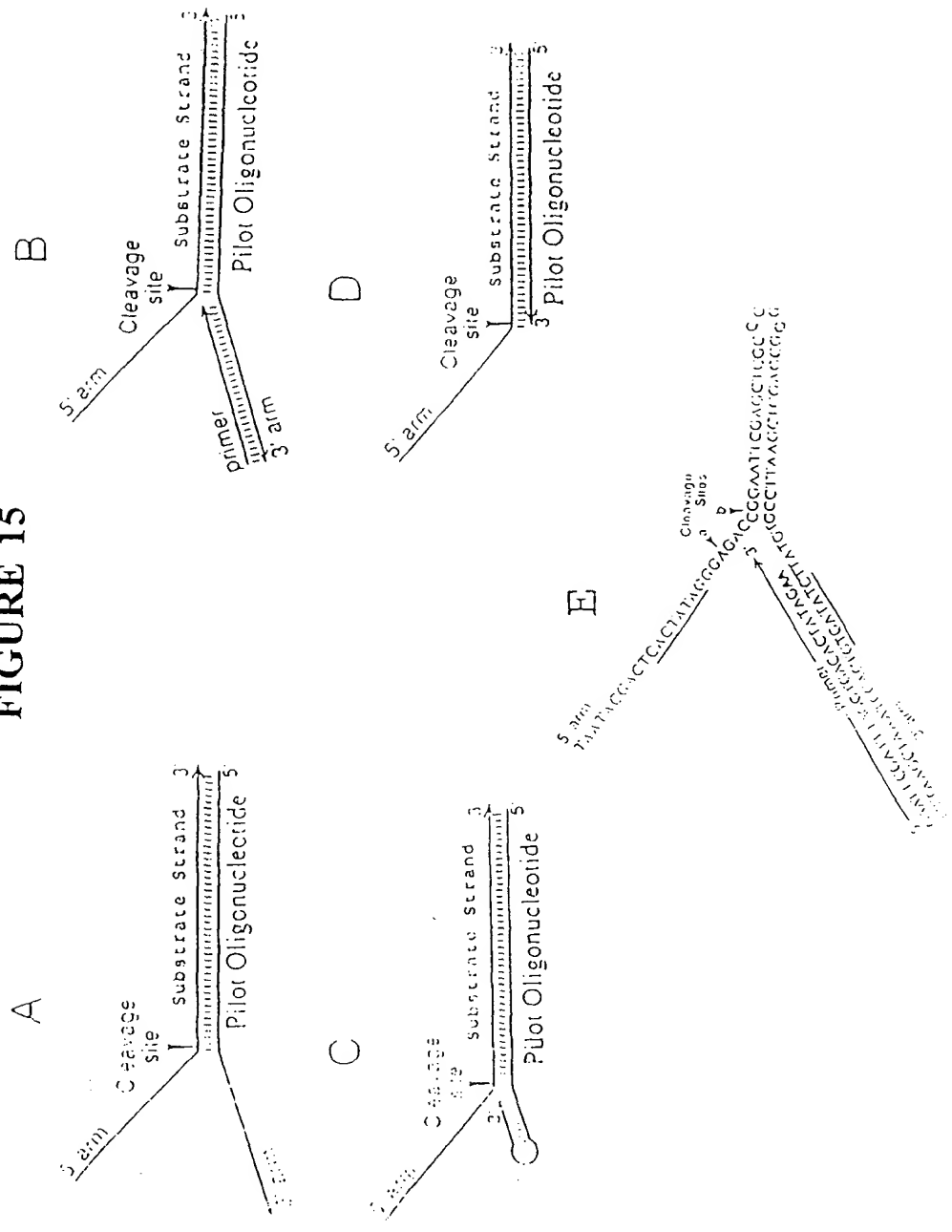
FIGURE 14



P<sub>ϕ10</sub>: Bacteriophage T7 ϕ10 promoter  
T<sub>0</sub> T7 ϕ Terminator  
RBS: Ribosome binding site

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FIGURE 15





5/1/5e

60311-10311

1 2 3 4 5 6 7

UNCLEAVED SUBSTRATE

CLEAVED SUBSTRATE

-	-	-	+	-	-	+	dNTPs
-	-	+	+	-	-	+	PRIMER
Taq	4e			5b			ENZYME

FIGURE 16

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UNINCORPORATED

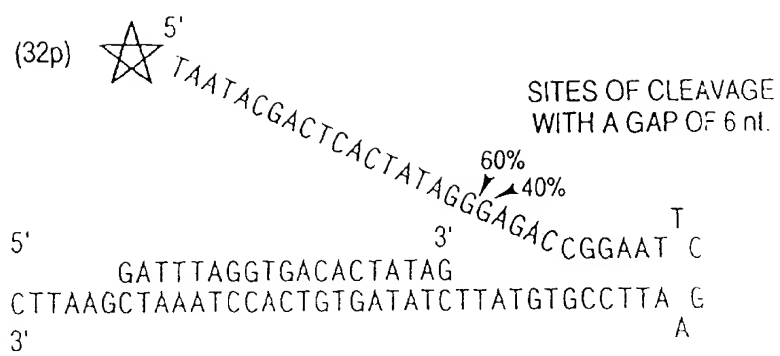


INCORPORATED  
32P dCMP



ENZYME	Taq	-	Taq	4b	4c	4d	4e	4f
PRIMED M13	-	+	+	+	+	+	+	+

FIGURE 17



**FIGURE 18A**

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				"4b"		UNMODIFIED	
				2 PT. MUTATION SMALL ACTIVITY		DNAP Taq	
				NO POL. ACTIVITY			
1	2	3	4	5	6	7	8
-	-	+	+	-	+	-	+

dNTP

34 NUC. —————

← HAIRPIN TEST MODULE

← CONVERSION TO DOUBLE STRANDED (COMPLETE EXTENSION OF PRIMER)

DESIRED PRODUCT 21 NUC. —————

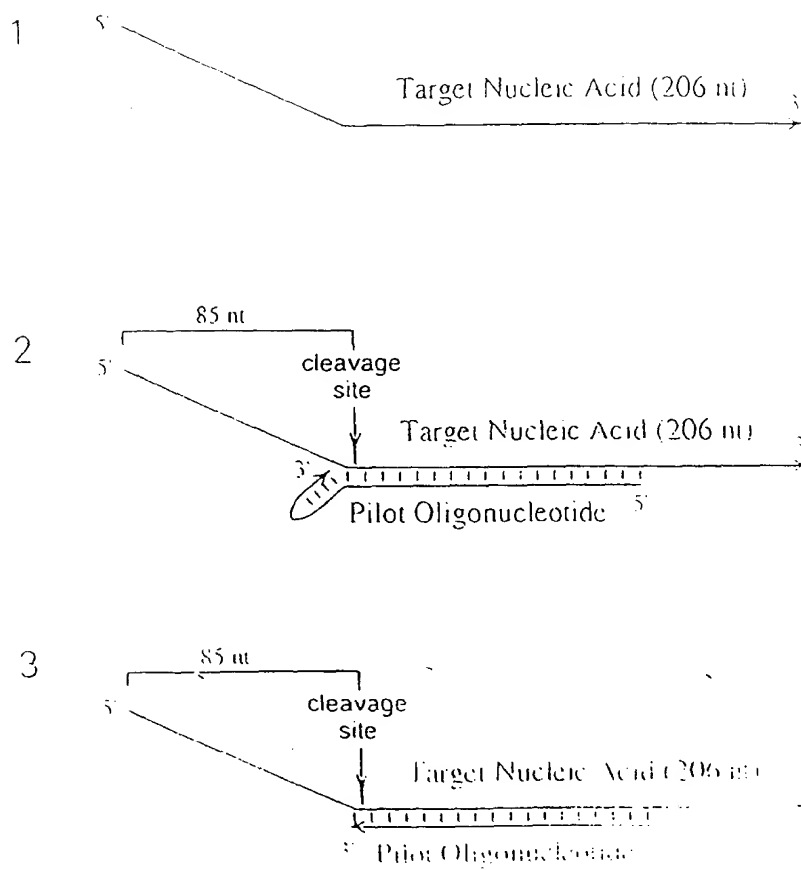
MULTIPLE BANDS CAUSED BY POLYMERIZATION

↑ SOME ABERRANT CLEAVAGE WITH "4b" BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

FIGURE 18B

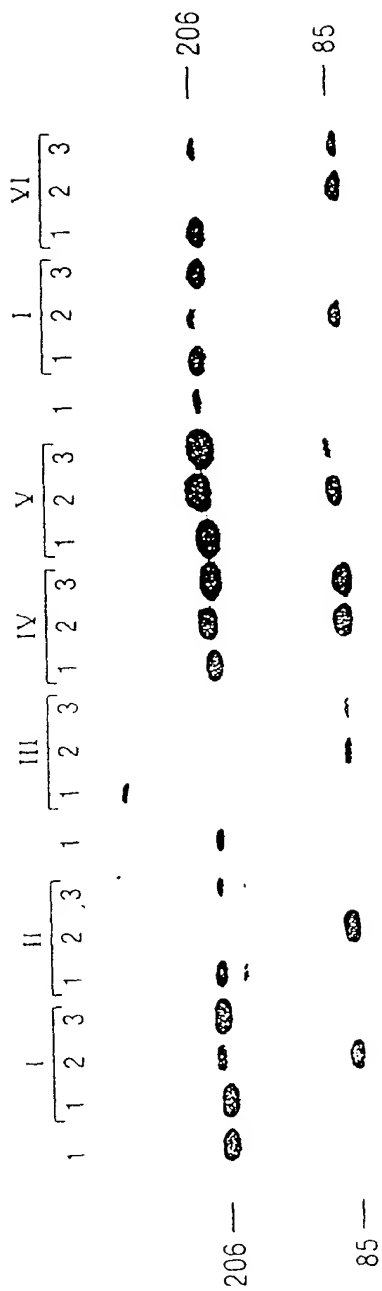


**FIGURE 20A**



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**FIGURE 20B**

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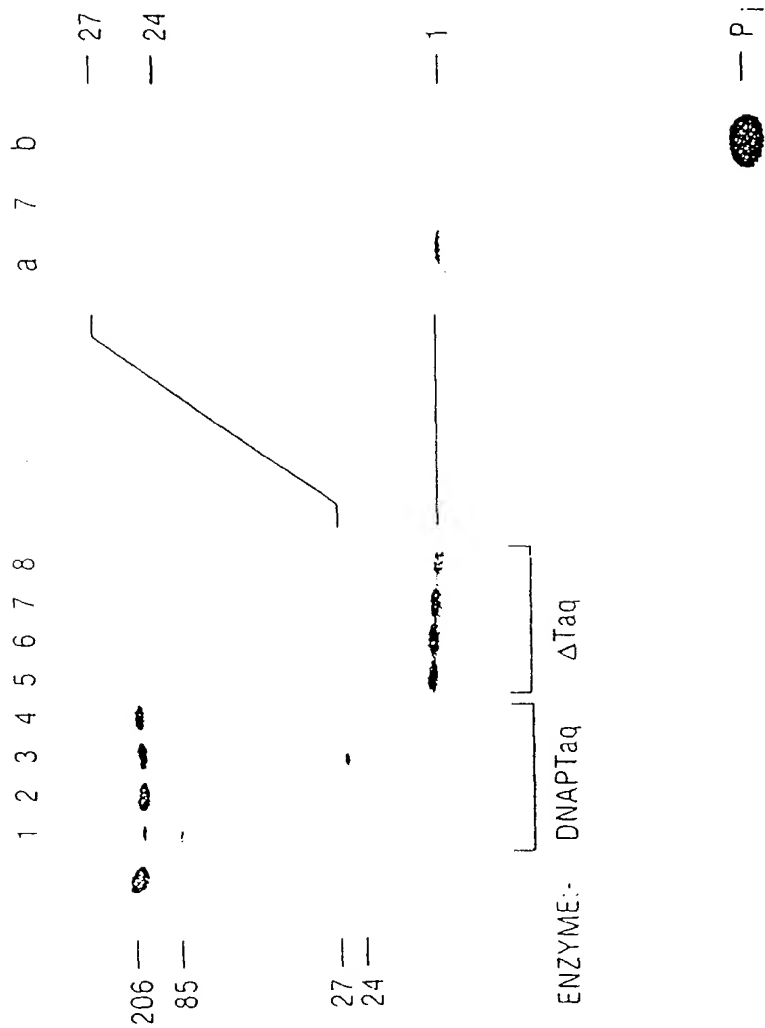


FIGURE 21A

FIGURE 21B



Handwritten text: 35/165'

FIGURE 22A

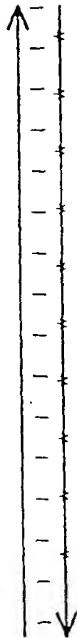


FIGURE 22B

\* = 32p

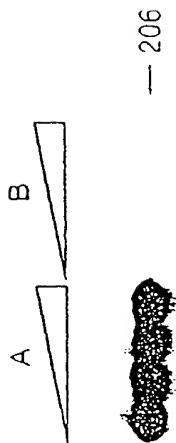
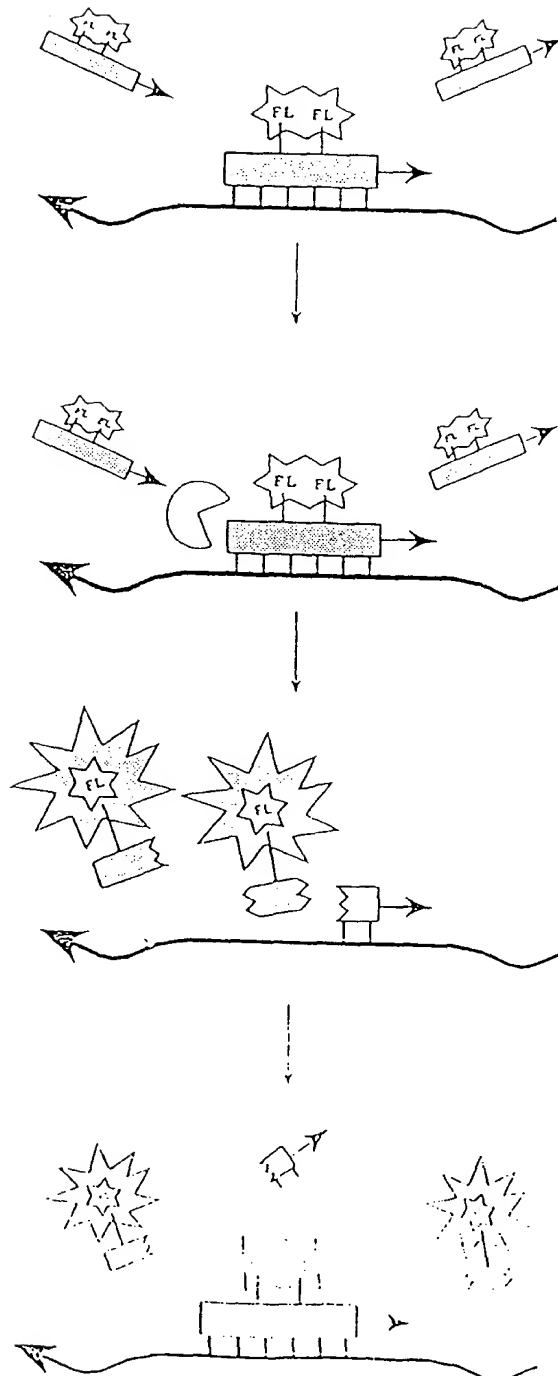
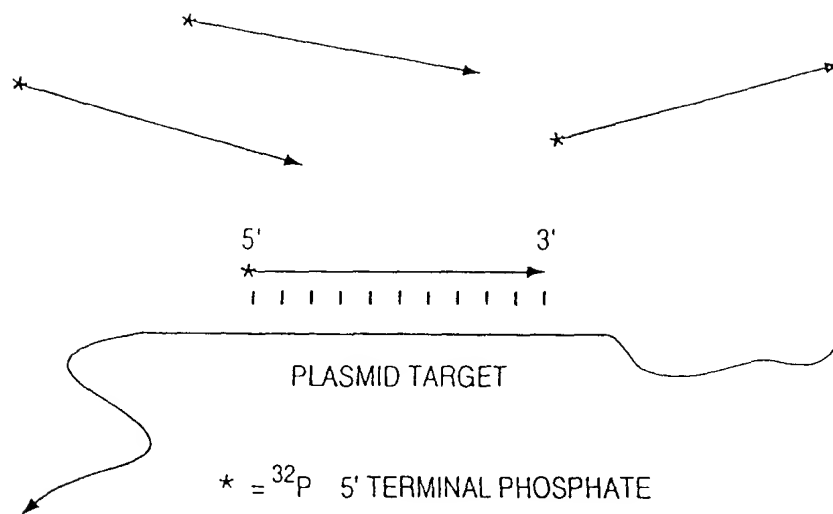


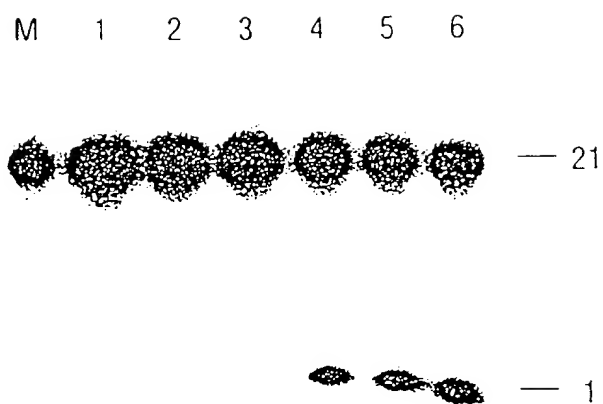
FIGURE 23



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**FIGURE 24A**

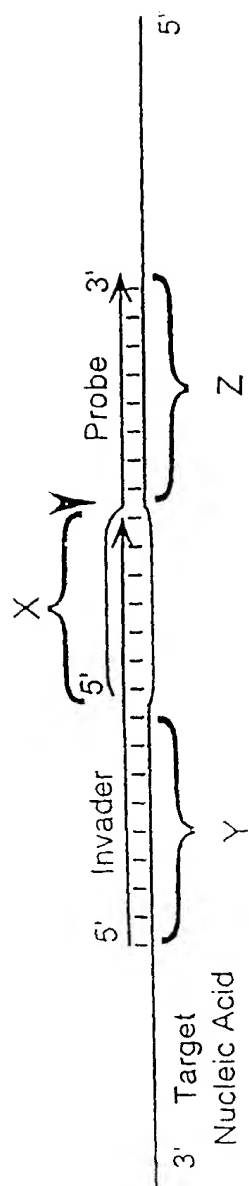


**FIGURE 24B**

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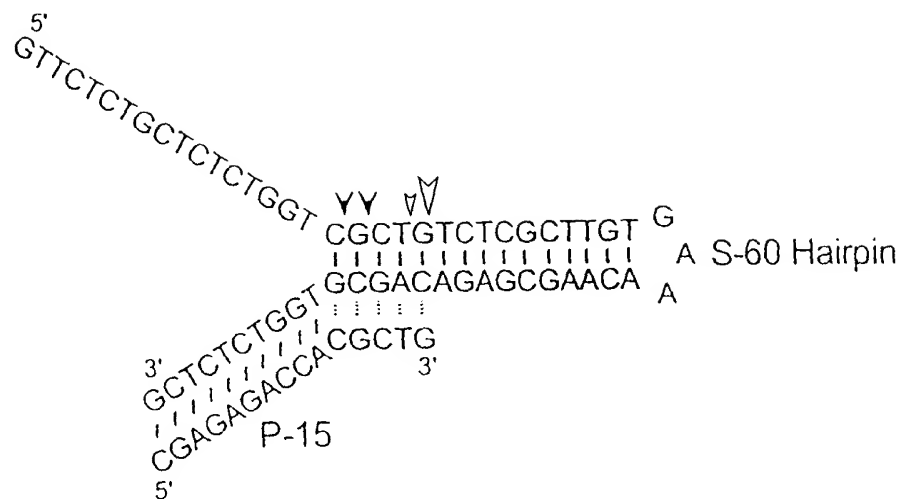
the target and the invader and the probe and the target

FIGURE 25



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FIGURE 26



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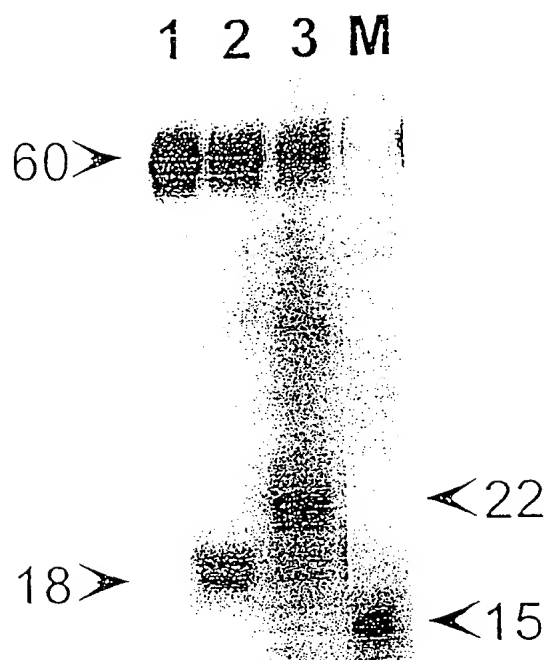


FIGURE 27

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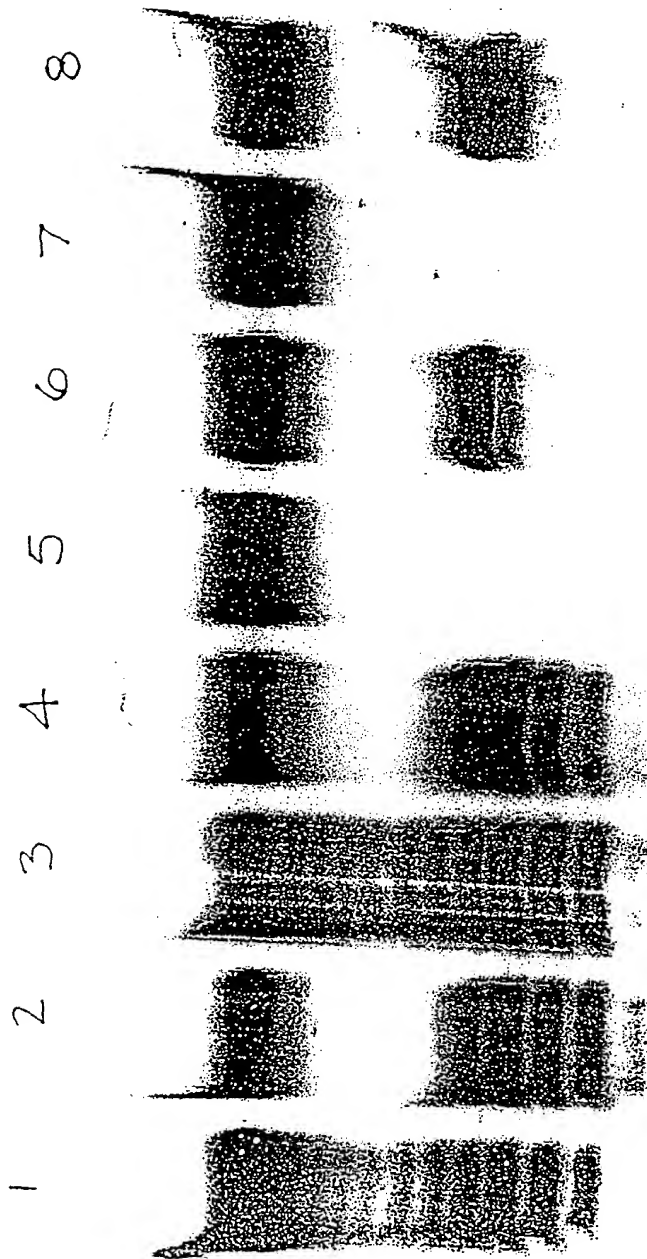




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CONFIDENTIAL

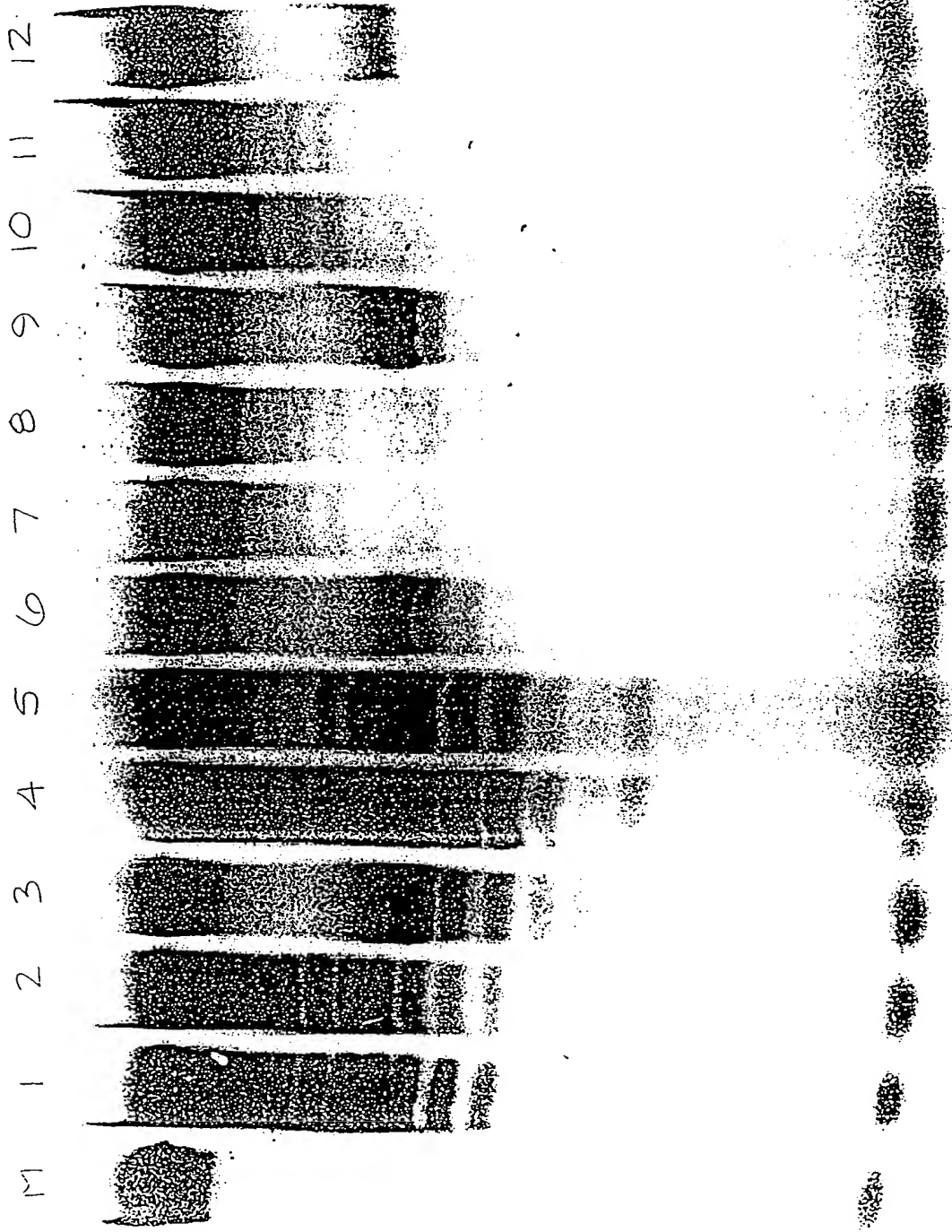
FIGURE 29



26A

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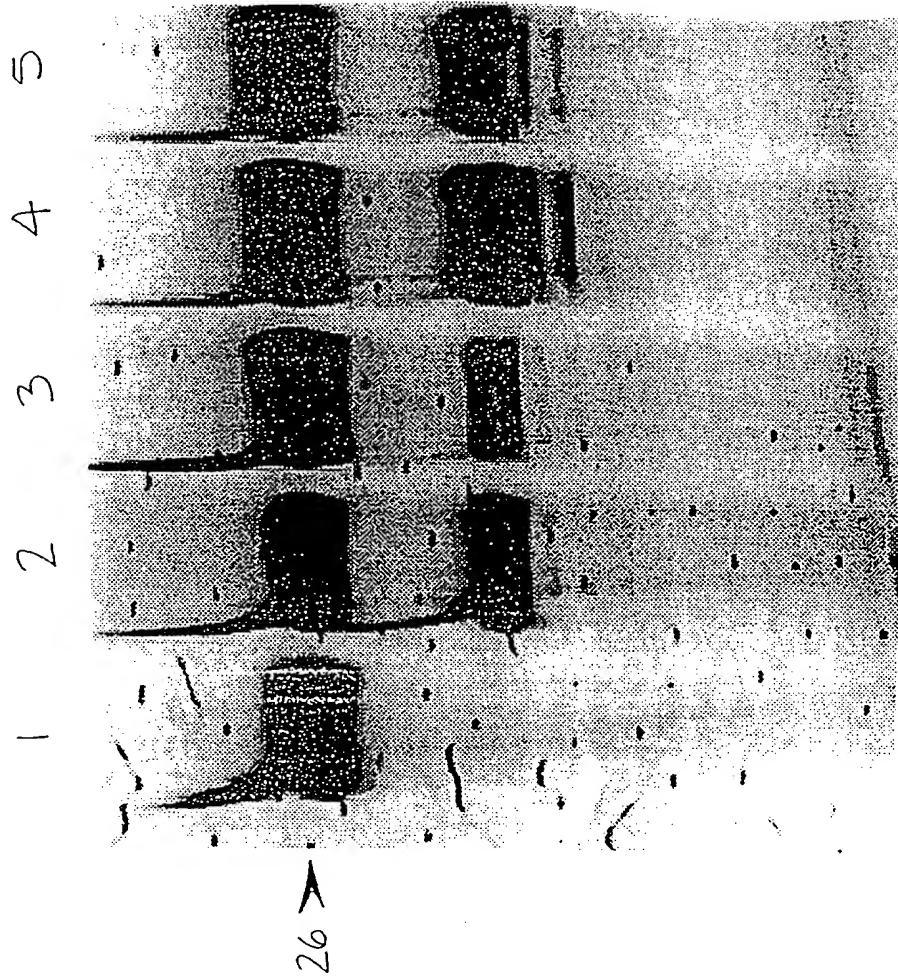
FIGURE 30



A

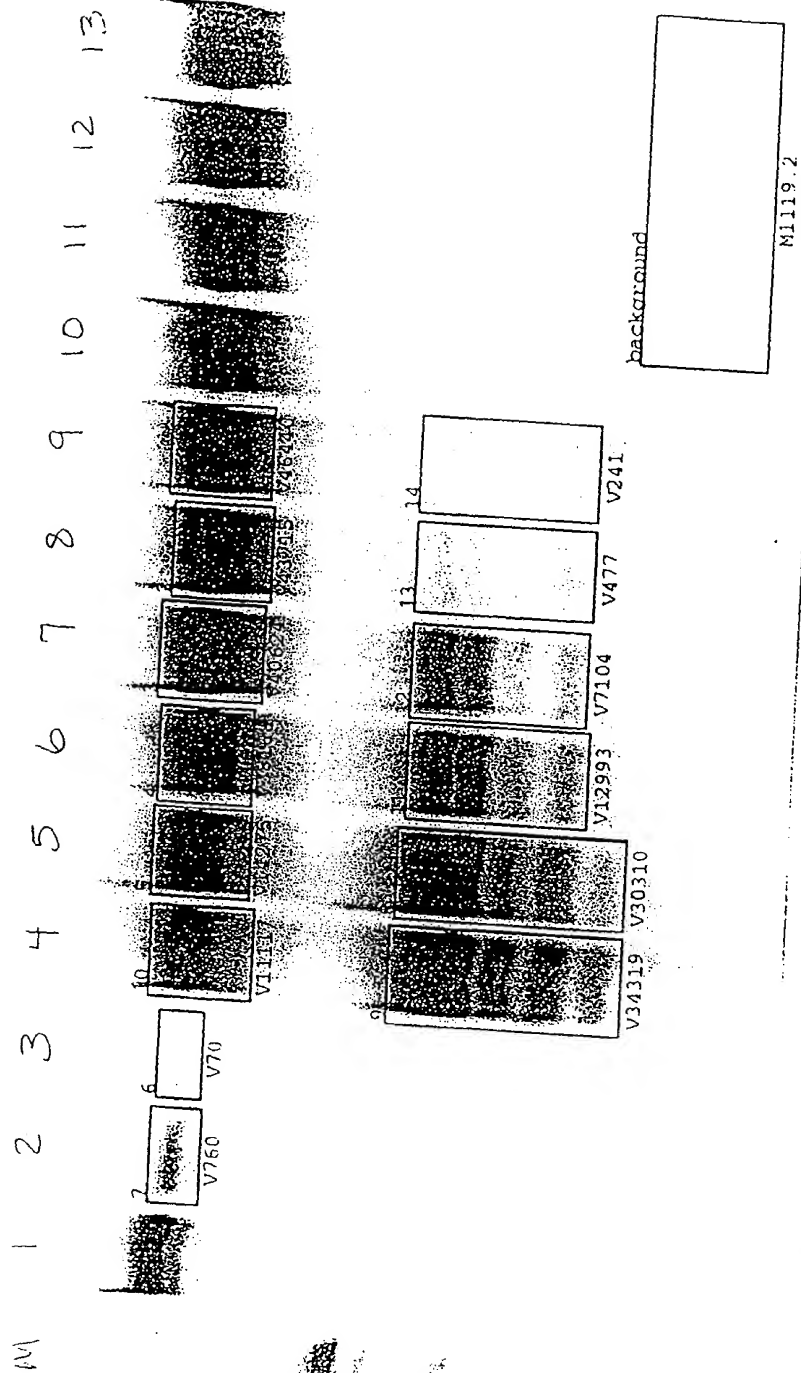
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FIGURE 31



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FIGURE 32



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SECRET

FIGURE 33

1 2 3 4 5 6 7 8 9 10 11



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DATE RECEIVED

FIGURE 34

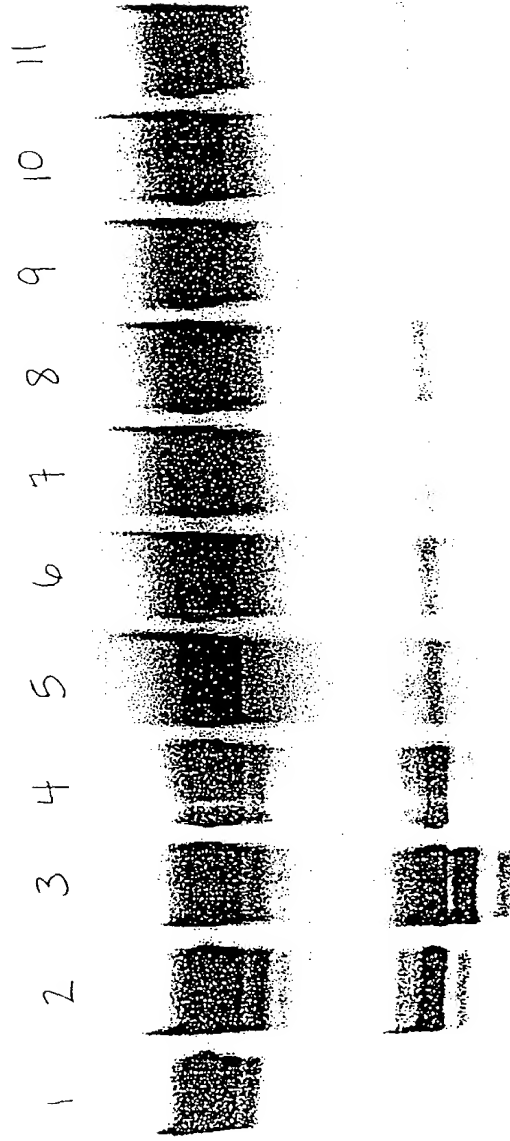
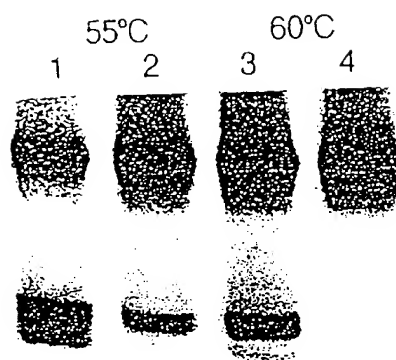


FIGURE 35



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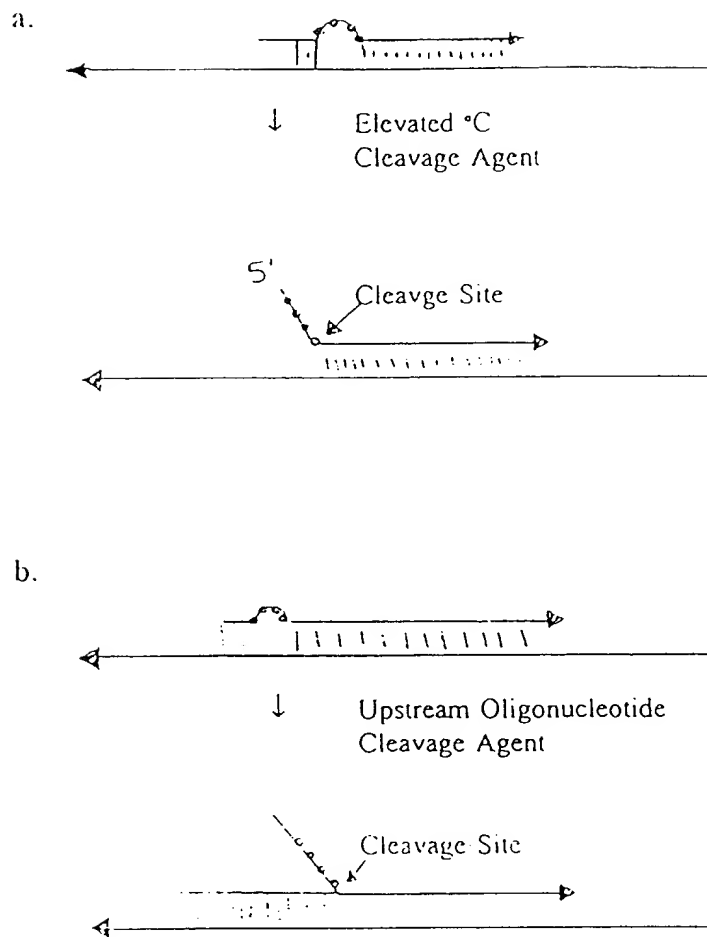


FIGURE 36

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59/6h

3'-ctgcccccttcg

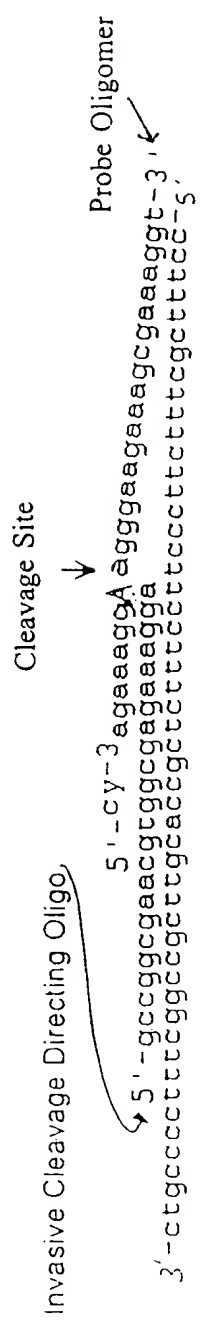
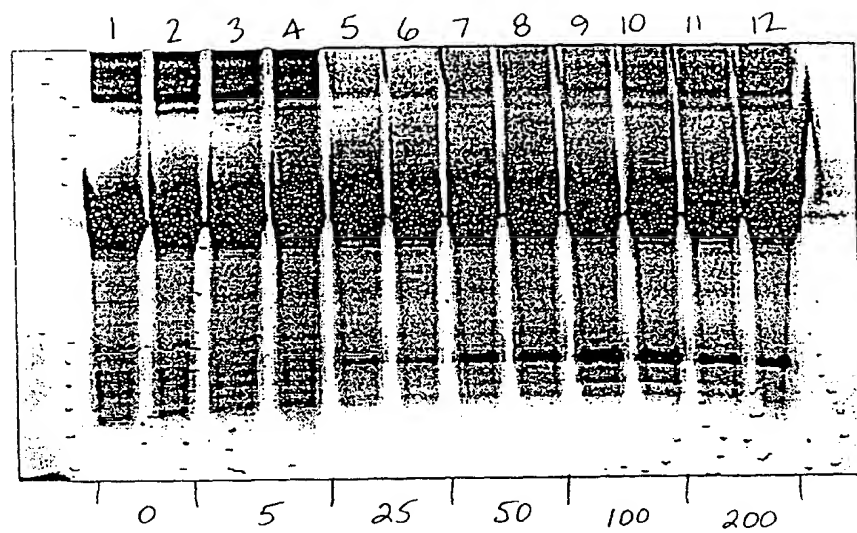


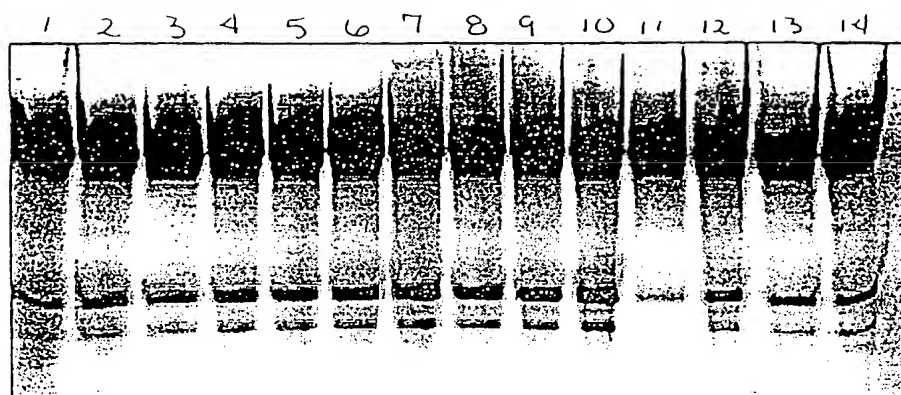
FIGURE 37

FIGURE 38



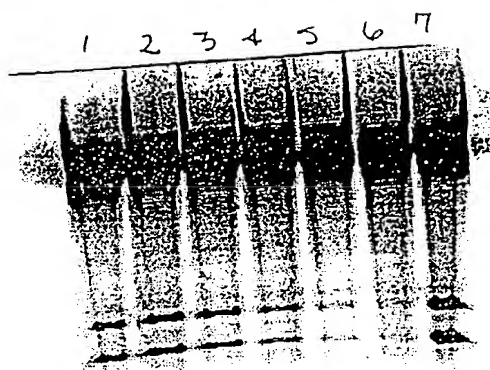
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FIGURE 39



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FIGURE 40



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FIGURE 41



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[illegible]

AG T7h

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inc/leaved

2019-2020

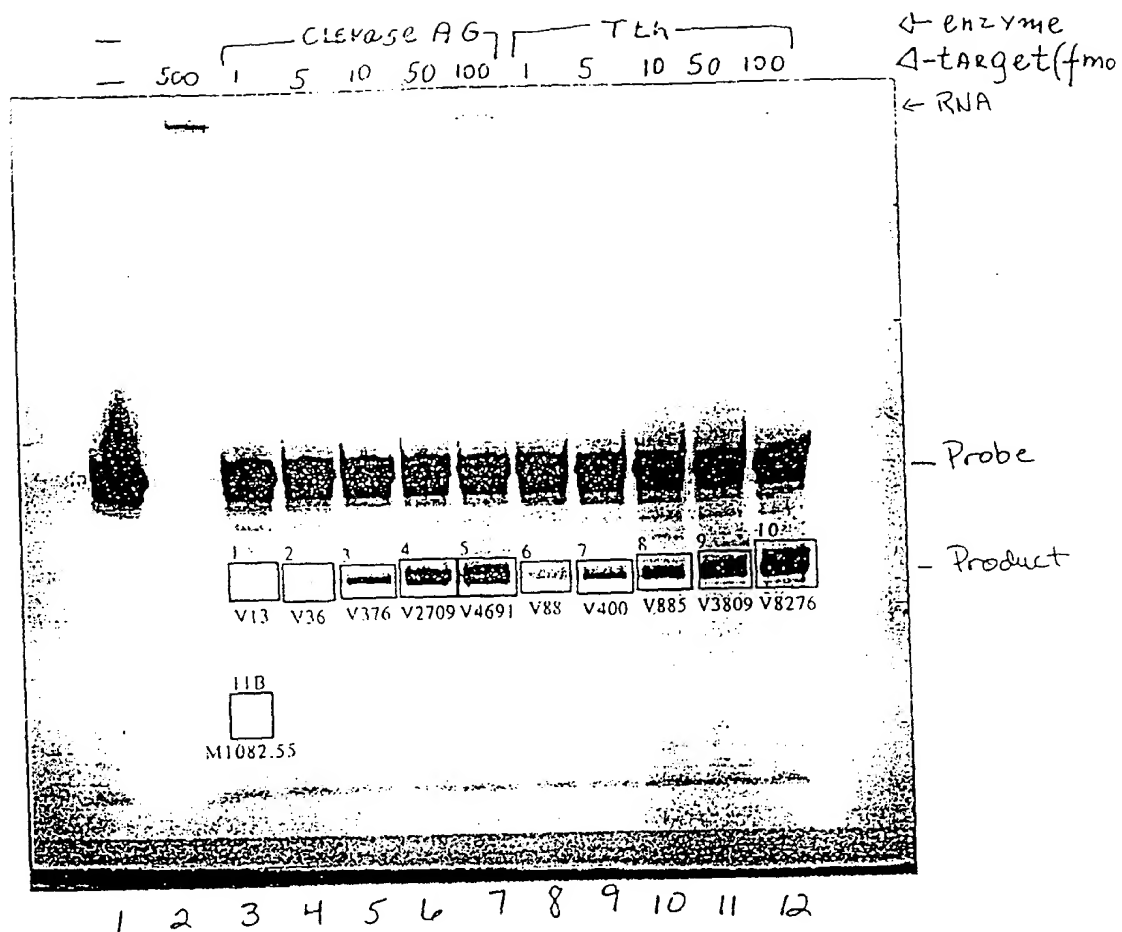


FIGURE 43

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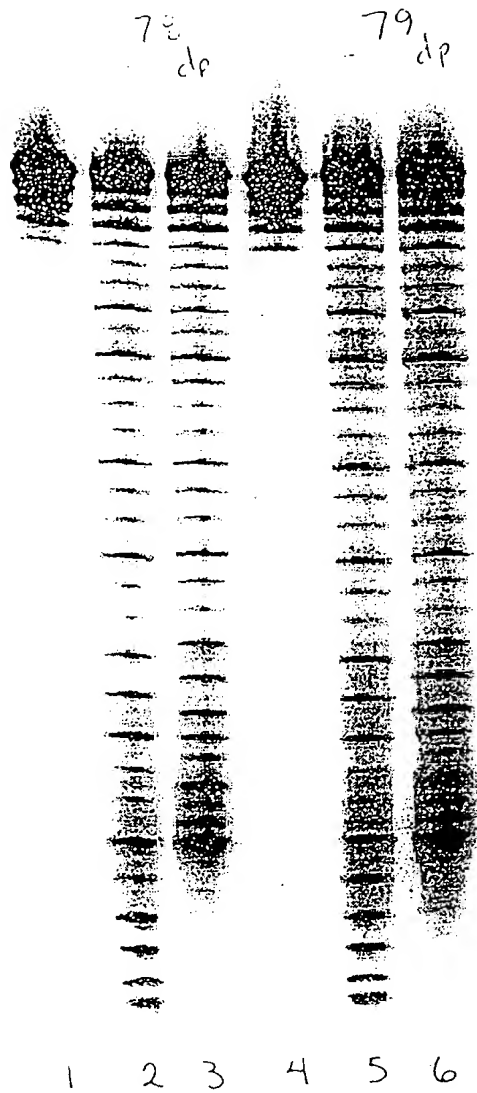


FIGURE 44

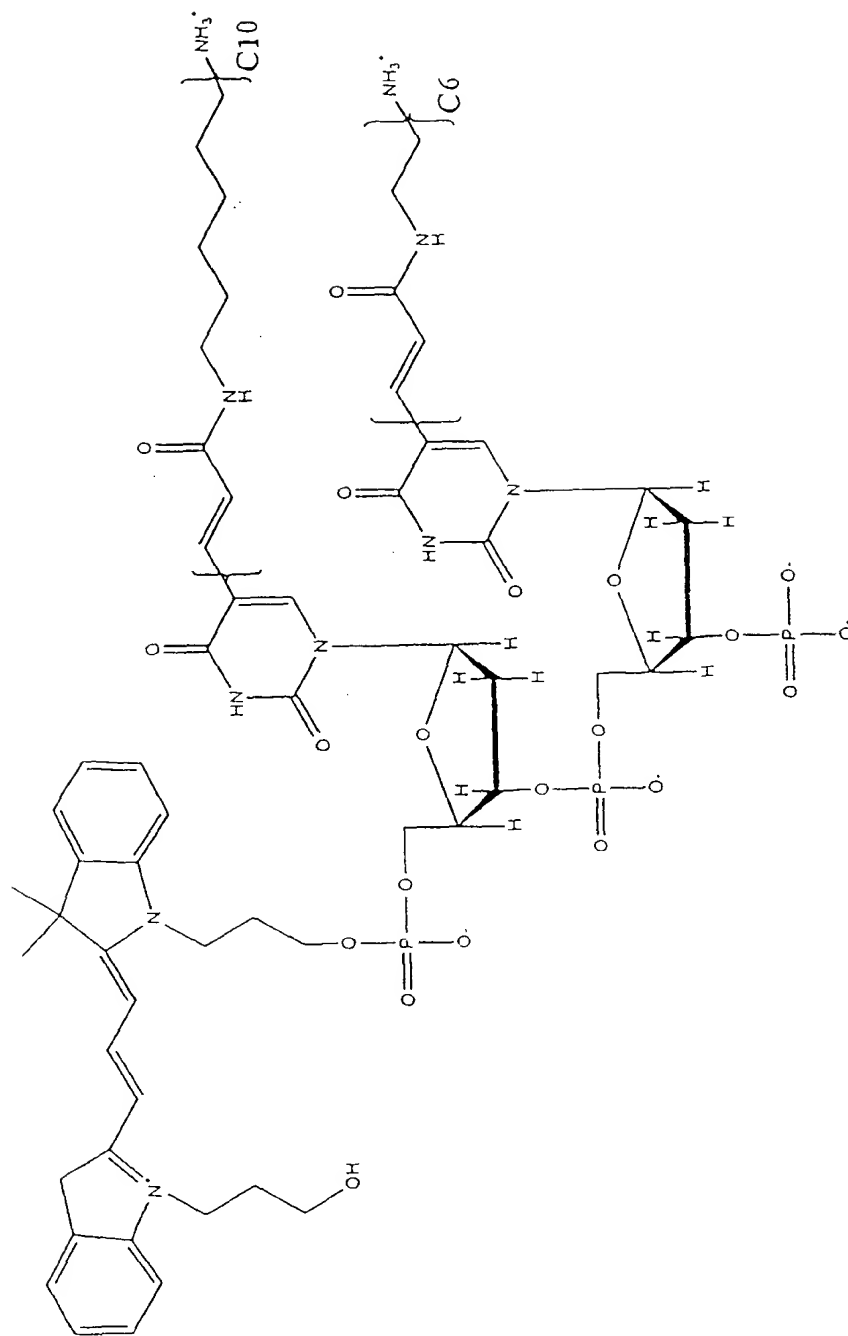
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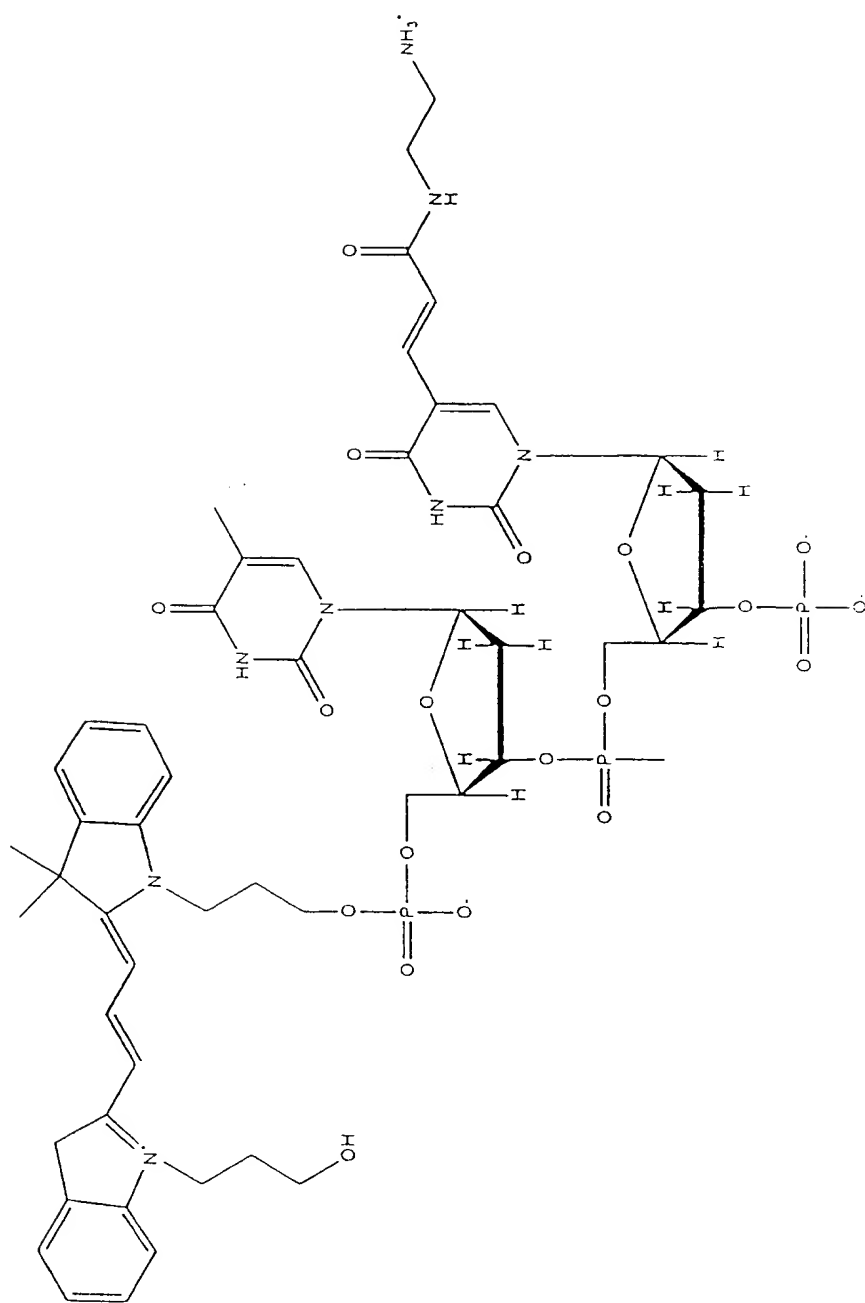
FIGURE 45

70 (C10 aminoT's)  
74 (C6 amino T's)



	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

75



[illegible]

97

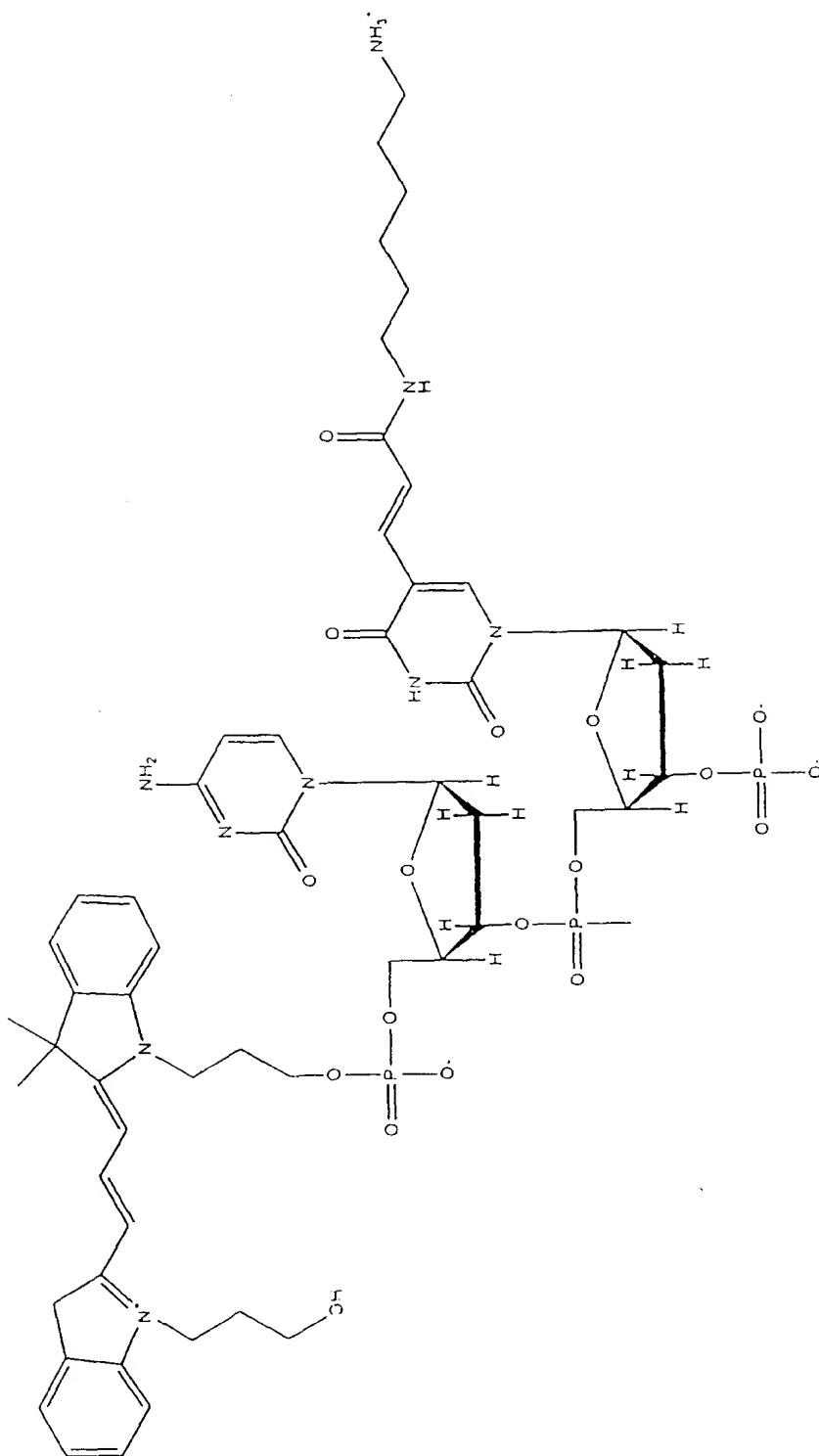
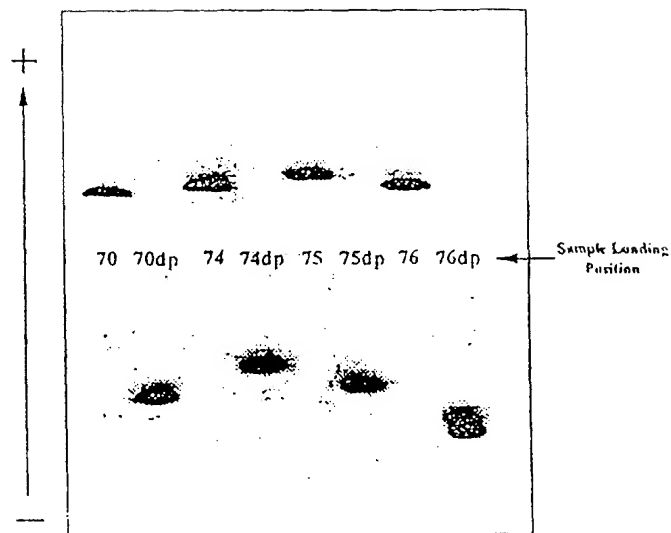
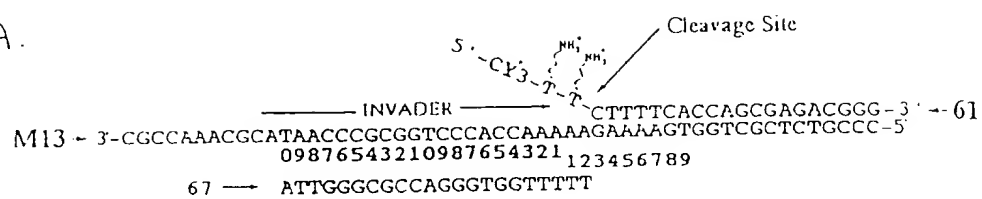


FIGURE 48



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A.



B.

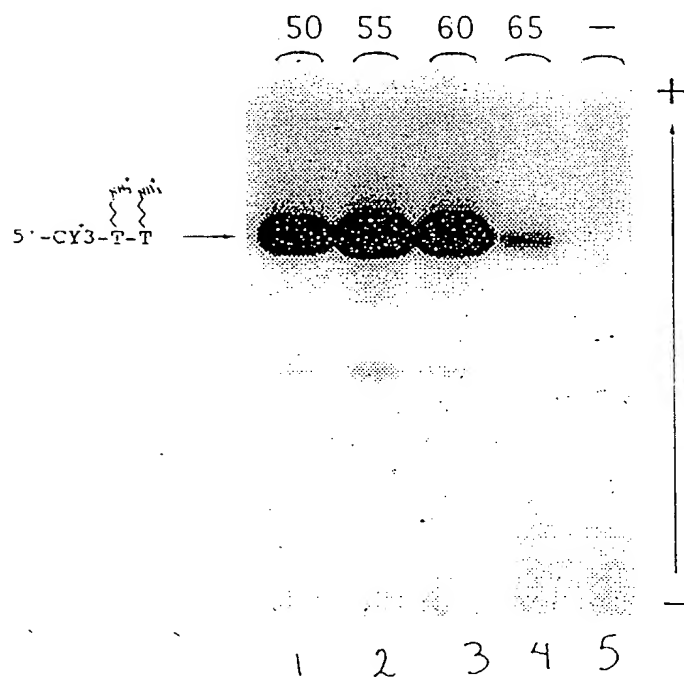
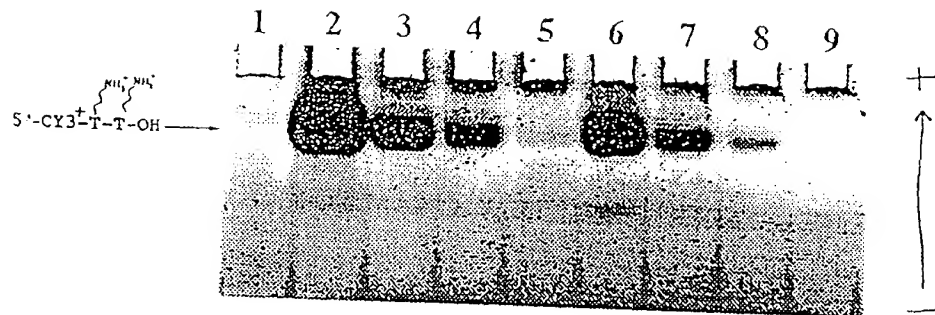


FIGURE 49

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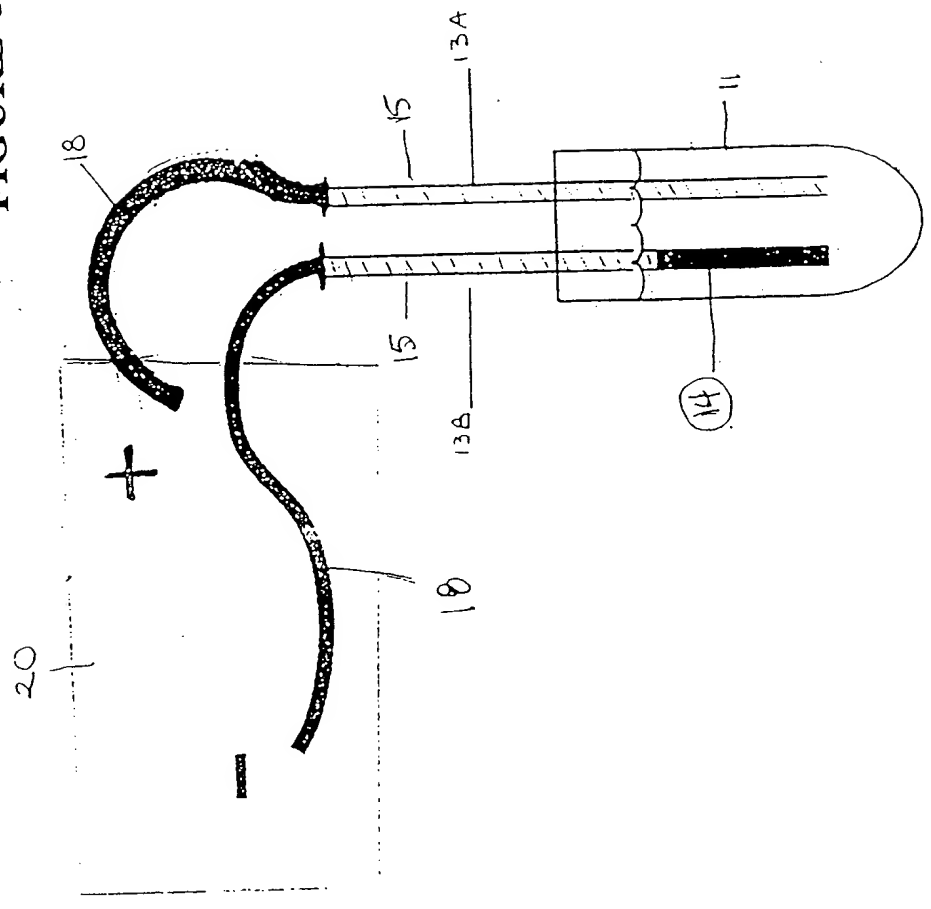
FIGURE 50



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FIGURE 51



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FIGURE 52

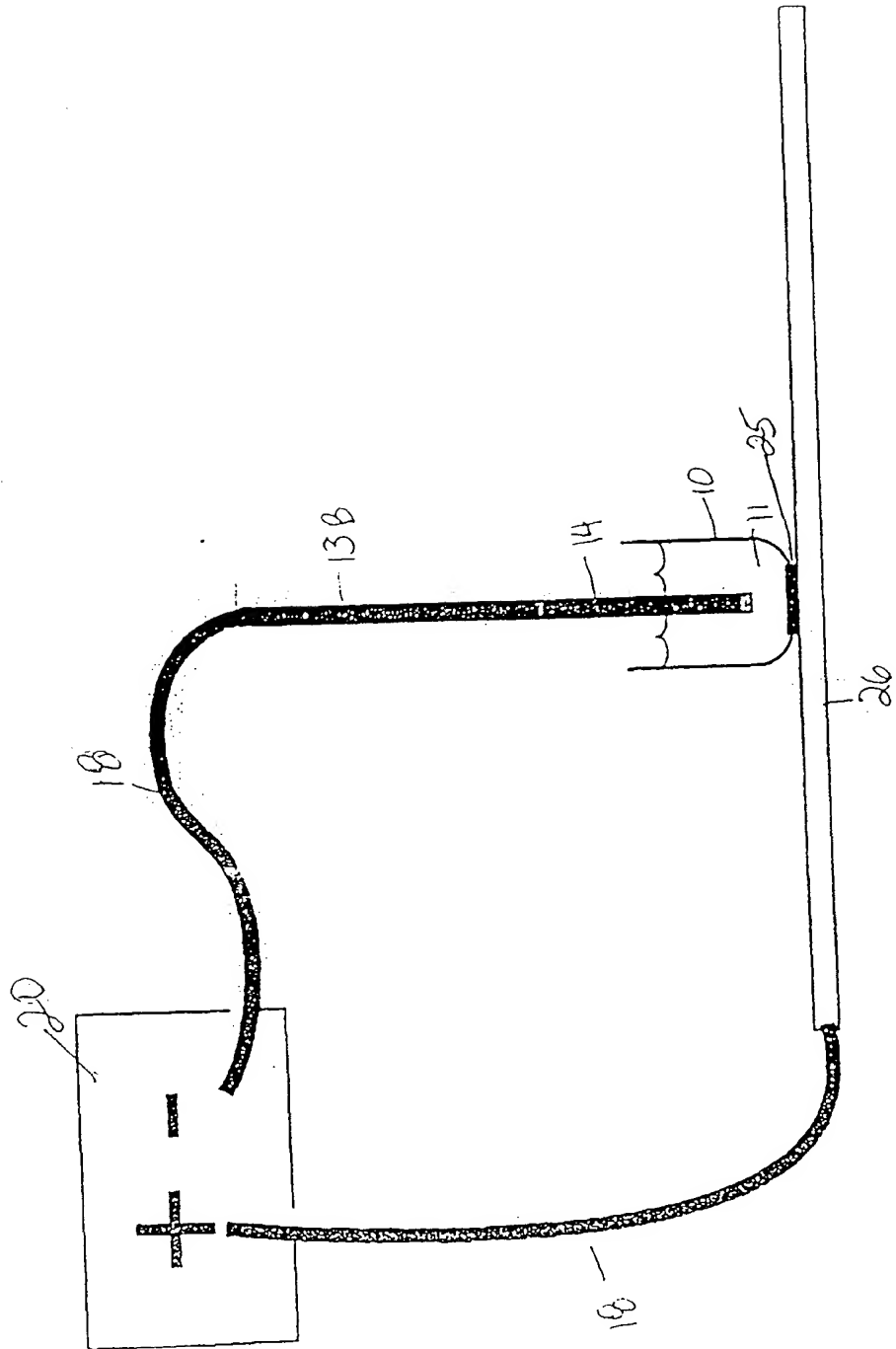
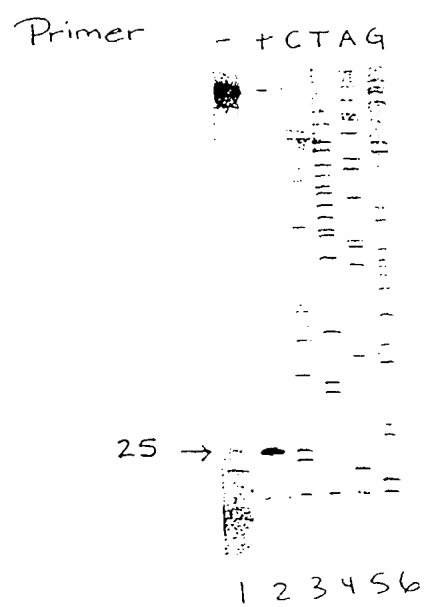




FIGURE 53



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5' AGAAAGGAAGGGAAGAAAGCGAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

AGAAAGGA  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

a

5' CAG AAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGAAGGA  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

b

5' CAGGG GGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGGGGGA  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

c

5' CAGGGTAC AGGGAAGAAAGCGAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

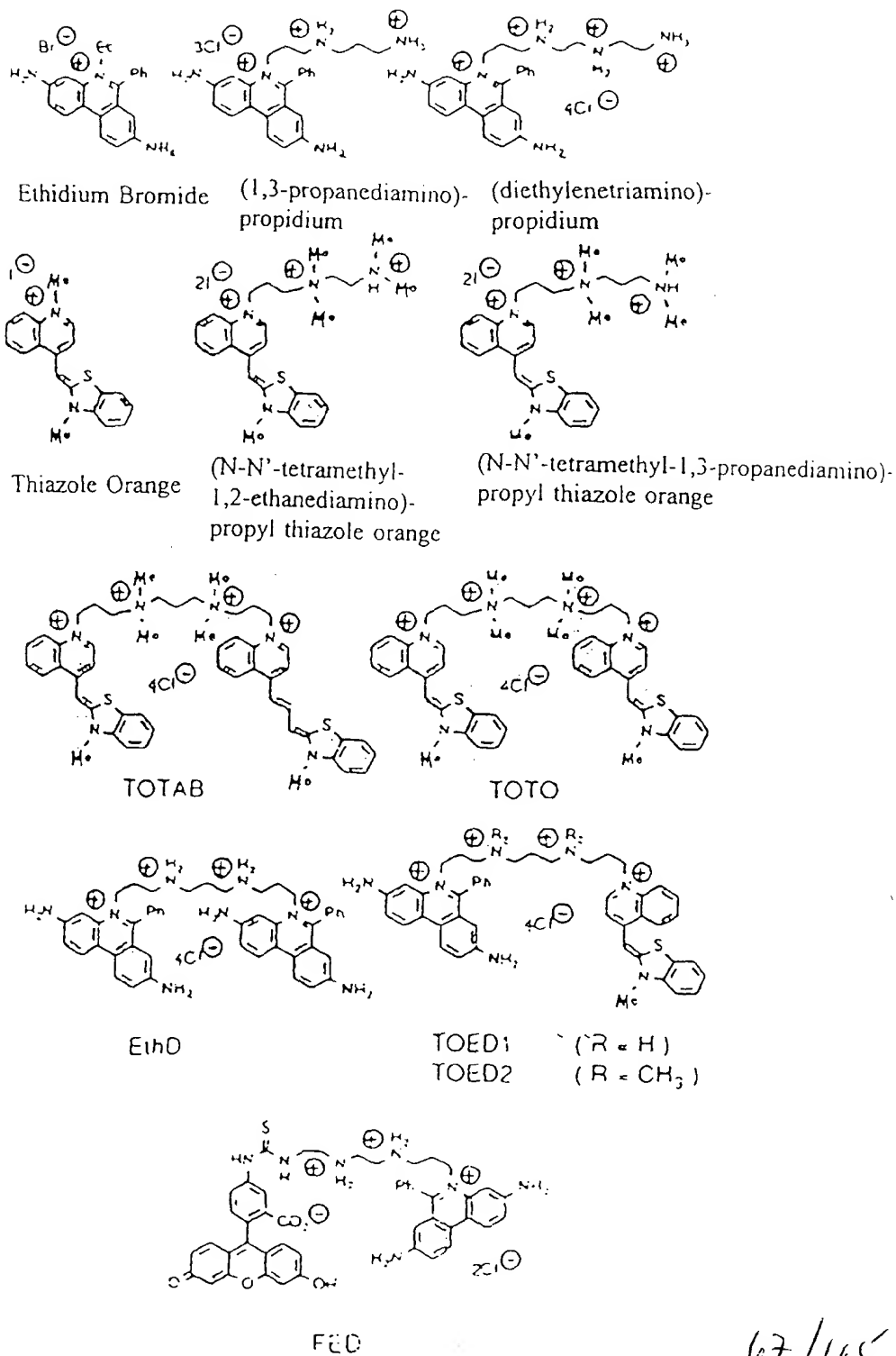
CAGGGTAC  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

d

FIGURE 54

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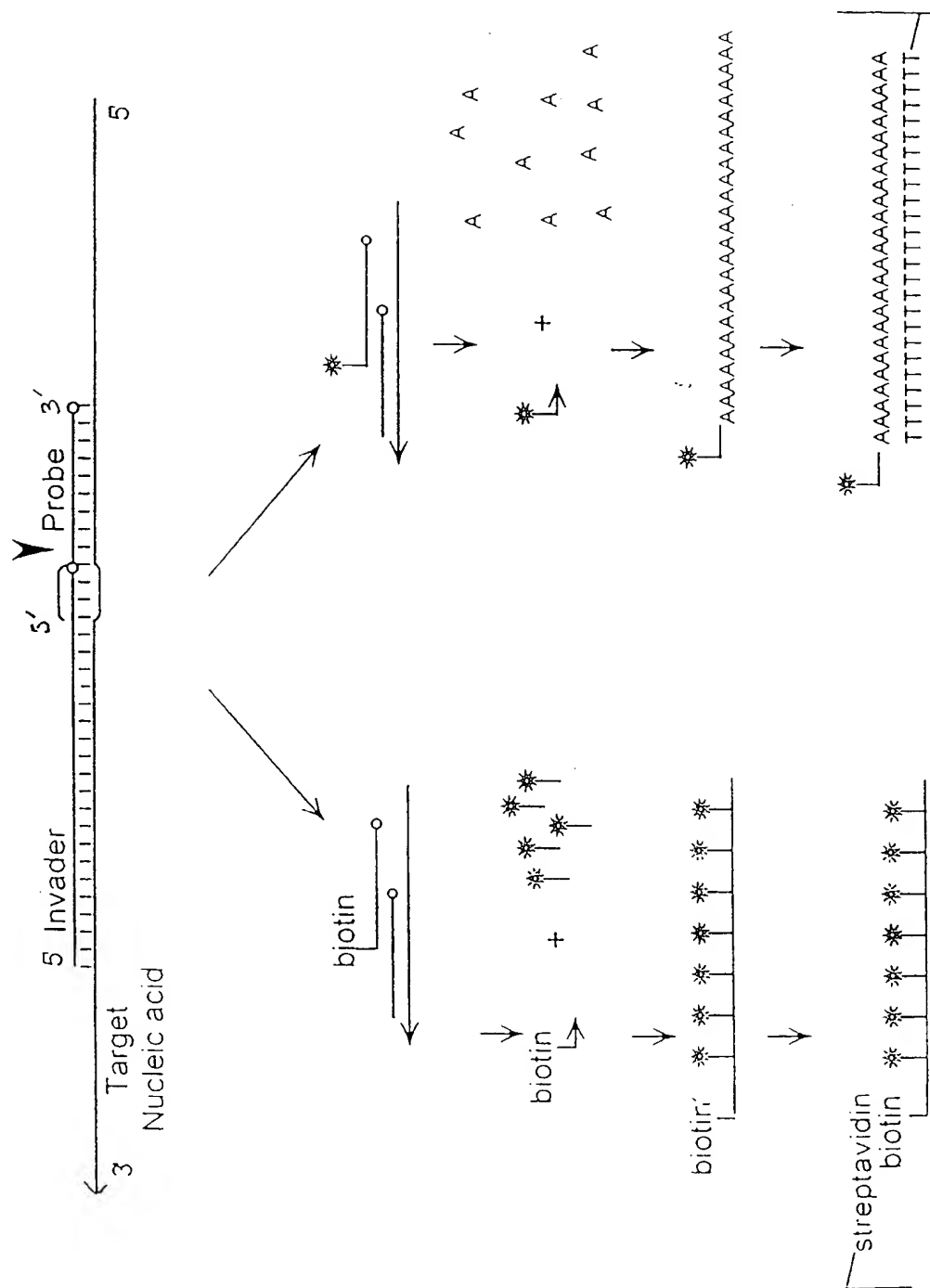
FIGURE 55



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FIGURE 56



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FIGURE 57

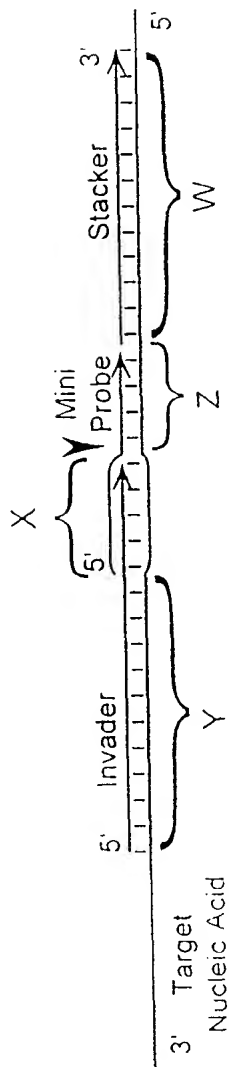
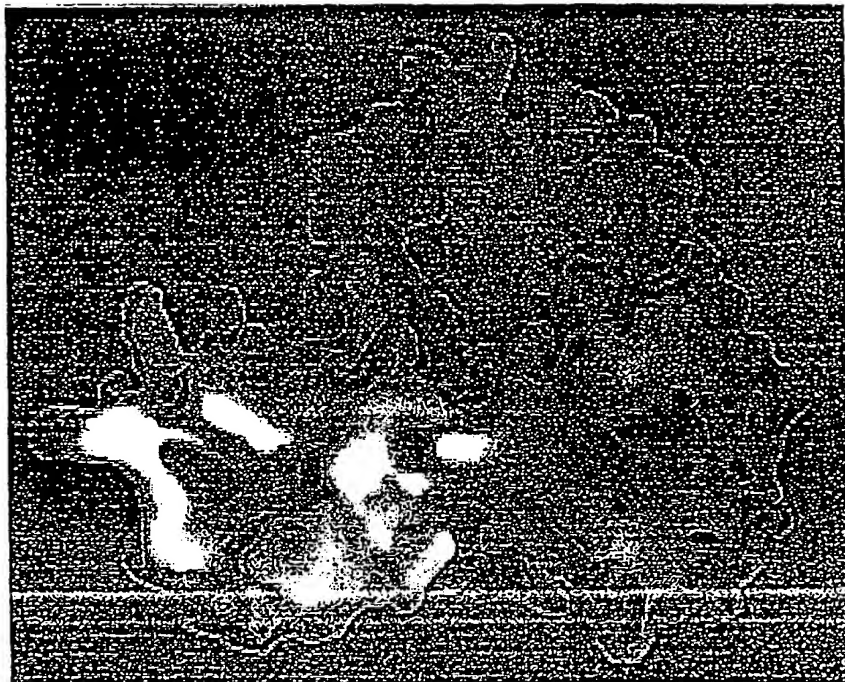


FIGURE 58



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[illegible]

**FIGURE 59A**

	20	30	40	50	60	70			
1	PGDFIPK	--NIISFEDLKGKKVAIDGMNAL	YOF	LT	SIRLDGSP	LRNRKGEITS	YNGVFY	MJAFENI	PRO
2	GEIIPR	--KEIELENLYGKKIAIDALNAI	YOF	LT	IROKDGTP	MDSKGRIT	SHLSGLFY	PFUFENI	PRO
3	IAOVAPSA	IRENDIKSYFGRKVAIDASMSI	YOF	IAVRO	-GGDV	LVONEEGETT	SHLMGMFY	HUMFENI	PRO
4	IAOVAPSA	IRENDIKSYFGRKVAIDASMSI	YOF	IAVRO	-GGDV	LVONEEGETT	S-LMGMFY	MUSFENI	PRO
5	IAOVAPSA	IRENDIKSYFGRKVAIDASMSI	YOF	IAVRO	-GGDV	LVONEEGETT	SHLMGMFY	YST510	PRO
6	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
7	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
8	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
9	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
10	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
11	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
12	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
13	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
14	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
15	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
16	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
17	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
18	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
19	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
20	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
21	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
22	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
23	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
24	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
25	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
26	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
27	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
28	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
29	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
30	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
31	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
32	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
33	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
34	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
35	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
36	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
37	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
38	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT	SHLMGMFY	YSTRAD2	PRO
39	SEHWPSAIR	KSDIKSFFGRKVAIDASMSL	YOF	IAVRO	ODGGQLT	NEAGETT			

[illegible]

- 19/10 E.

150	160	170	180	190	200	210
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220	230	240	250	260	270	280
-----	-----	-----	-----	-----	-----	-----

```

-----PELIELNEVLDIRISLOQLIDIAIFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV MJAFEN1 PRO
VE--KPELILLEEVLKELKLTREKLIELAILVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF PFUFEN1 PRO
SRILGELGLNOEOFVOLCILLGSDYCESIRGIGPKRAVDL IOK--HKSIEEIVRRLDPN-----KY HUMFEN1 PRO
SRVLGELGLNOEOFVOLCILLGSDYCESIRGIGAKRAVDL IOK--HKSIEEIVRRLDPS-----KY MUSFEN1 PRO
TELVRGLDLTIEOFVOLCIMLGCDYCESIRGVGPVTALKLKT--HGSIEKIVEFIESGESNNTKW YST510 PRO
EASIEILKLLGLORKNMIELAOULLGSDYTNGLKGMGPVSSIEVIAEF--GNLKNFKDWYNNGOFDKRK YSTRAD2 PRO
HDDMKREFNVNOMDLIKLAHLLGSDYTMGLSRVGPVLALEILHEFPGOTGLFEFKKWFORLSTGHAS SPORAD13 PRO
EYDPTNOLGLORNKLINLAYLLGSDYTEGIPITVGCVTAMEILNEFPGHGLEPLLKFESEWHEAQKNP HUMXPG PRO
EYDPTNOLGLORNKLINLAYLLGSDYTEGIPITVGCVTAMEILNEFPGRGLDPLLKFESEWHEAQNNK MUSXPG PRO
EYDPTNOLGLORNKLINLAYLLGSDYIIGIPTVGYVVSAMEILNEFPGGGLEPLVKFEKWSEAOOKD XENXPG PRO
EYDPTNOLGLORNKLINLAYLLGSDYIIGIPTVGYVVSAMEILNEFPGGGLEPLVKFEKWSEAOOKD XENXPG PRO
-----SSTACLDHIMHLSGRMFM----- CELRAD2 PRO

```





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-30	440	450	460	470	480	490
MJAFEN1 PRO						
PFUFEN1 PRO						
HUMFEN1 PRO						
GSL S						
MUSFEN1 PRO						
YST510 PRO						
YSTRAD2 PRO						
SPORAD13 PRO						
HUMXPG PRO						
MUSXPG PRO						
XENXPG PRO						
CELRAD2 PRO						

-30	510	520	530	540	550	560
NKTKOKTL						
KSGKOSTL						
KKAKTGAAG						
KKAKTGAC						
NKKLNKNKN						
PREYISGOKKLNTSKRISTATGKL						
PKTNSSSISIENLPRTKLSLL						
TSSSDSDDDGGKEKMVLVTARSVFGKKRRKLRRARG						
VSTARVFGKKRRKLKSMK -						
AKPVFOGKKT SKTMKE						
RSVKIRAFKPYPTDVI						

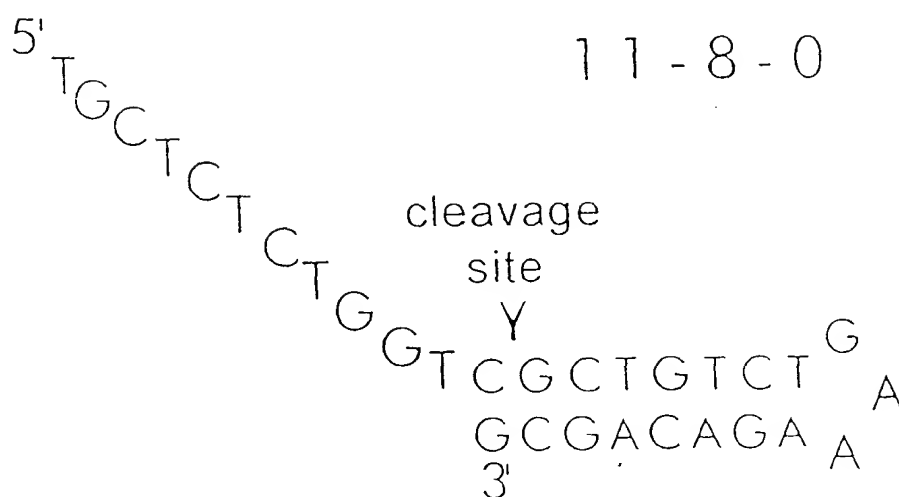
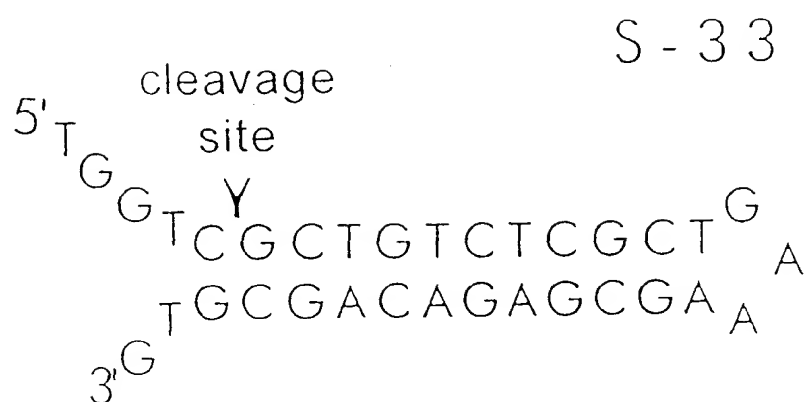
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# FIGURE 59E

MJAFEN1 PRO  
PFUFEN1 PRO  
HUMFEN1 PRO  
MUSFEN1 PRO  
YST510 PRO  
YSTRAD2 PRO  
SPORAD13 PRO  
HUMXPG PRO  
MUSXPG PRO  
XENXPG PRO  
CELRAD2 PRO

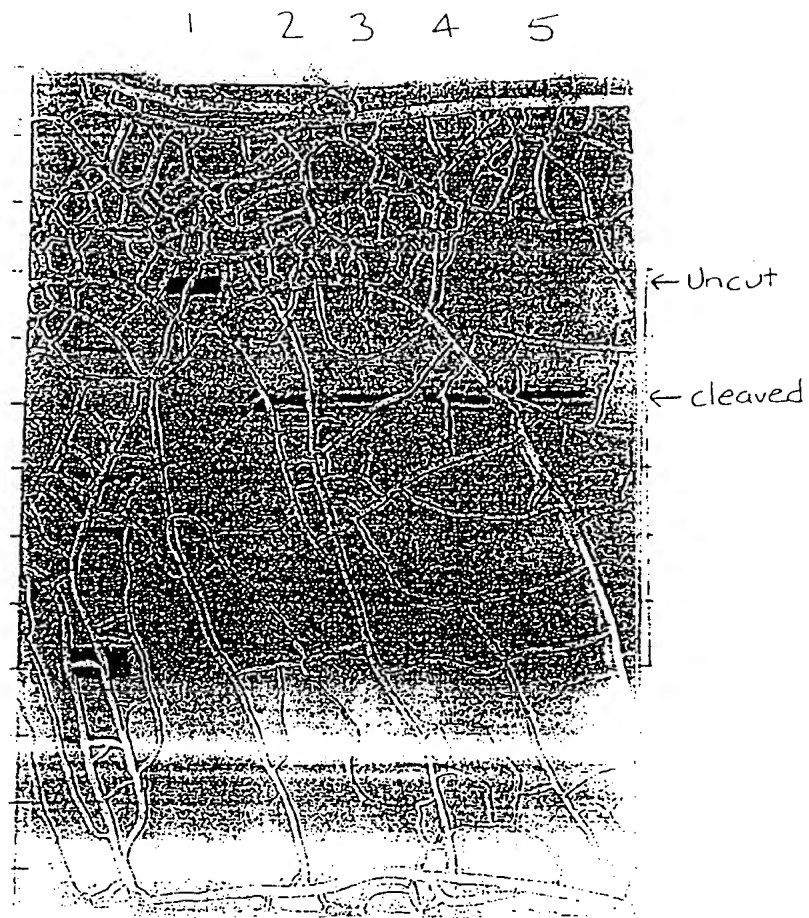
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIGURE 60



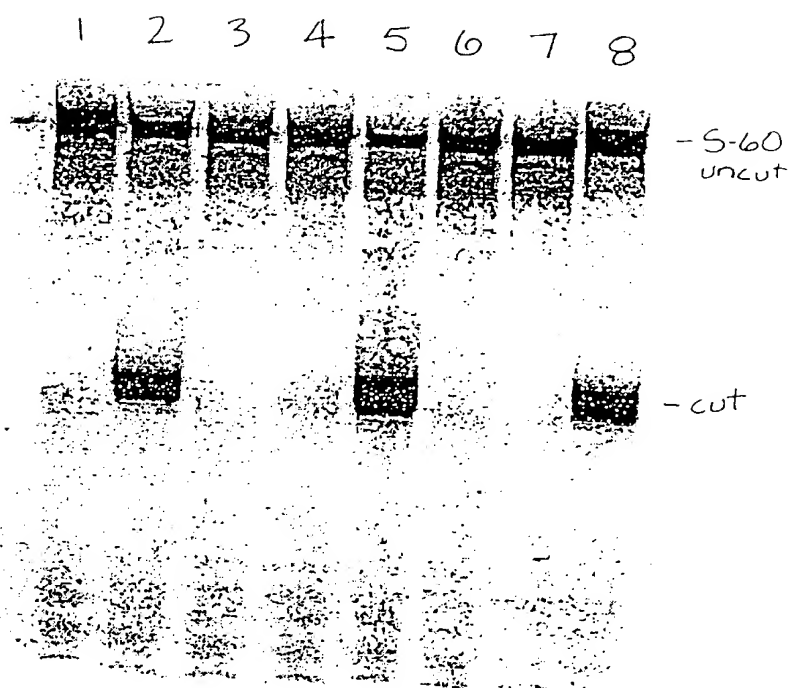
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FIGURE 61



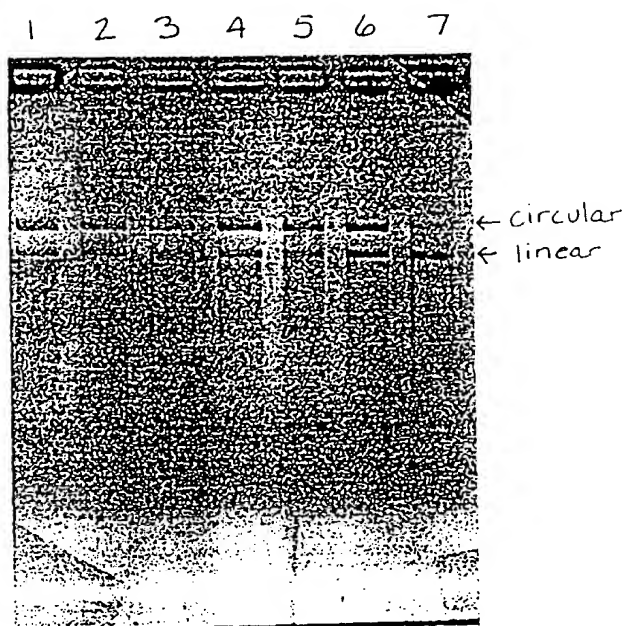
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FIGURE 62

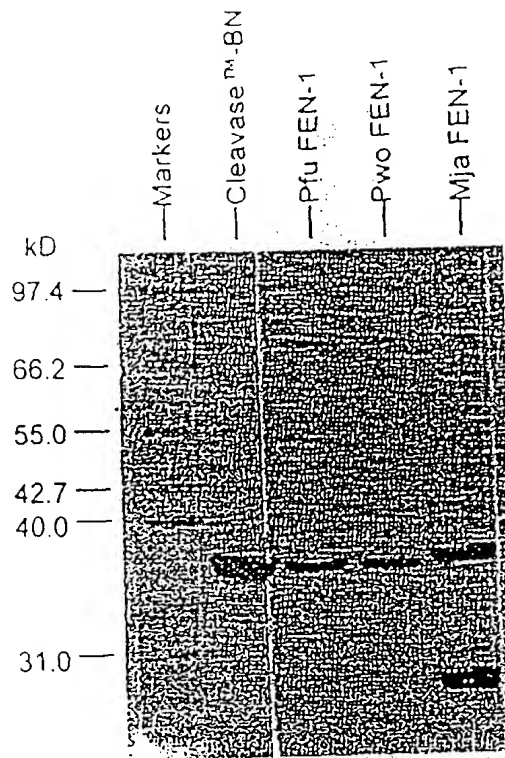


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FIGURE 63



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**FIGURE 64**

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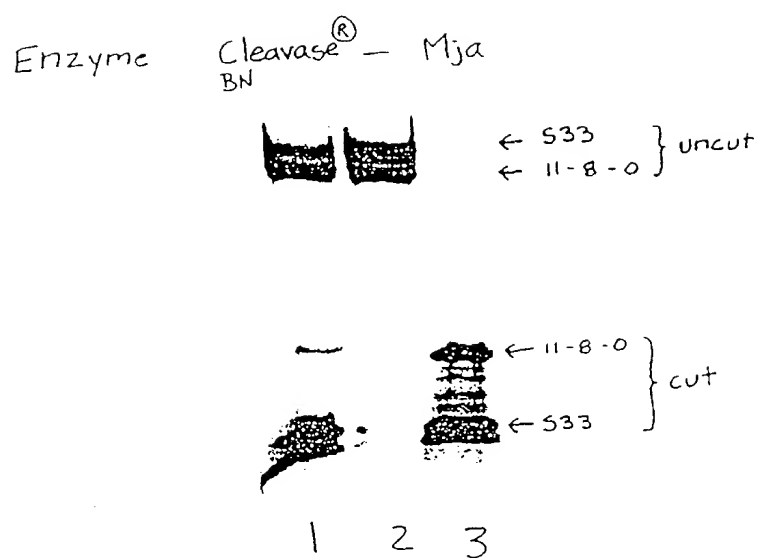


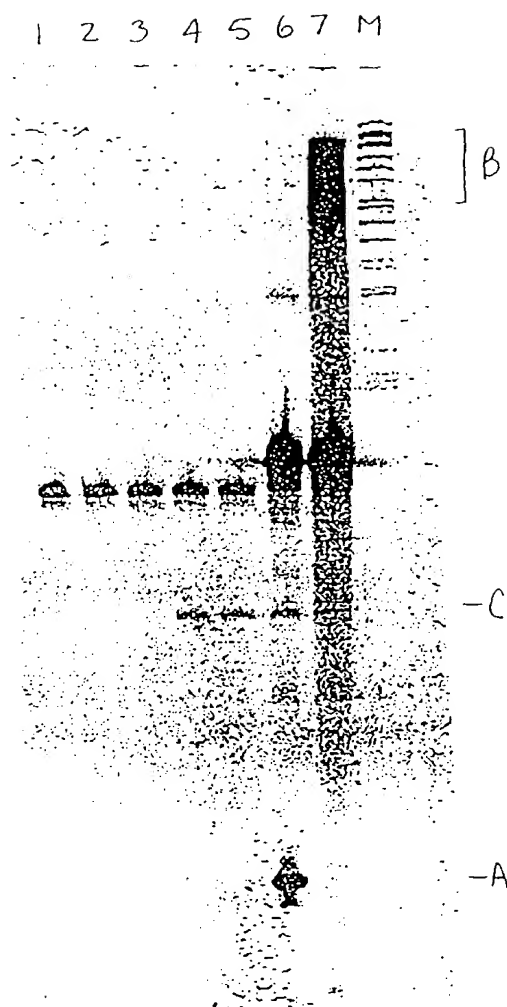
FIGURE 65

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The figure displays three vertical lanes of gel electrophoresis results. Each lane contains multiple horizontal bands of varying intensity and thickness. The bands are labeled vertically along the left side of each lane with letters G, A, C, and T, indicating specific nucleotide sequences or markers. The top lane shows a dense pattern of bands, while the middle and bottom lanes show more distinct, separated bands.

5'-nAGAAggaagggga agaaagcgaagG-3'

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**FIGURE 67**

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FIGURE 68

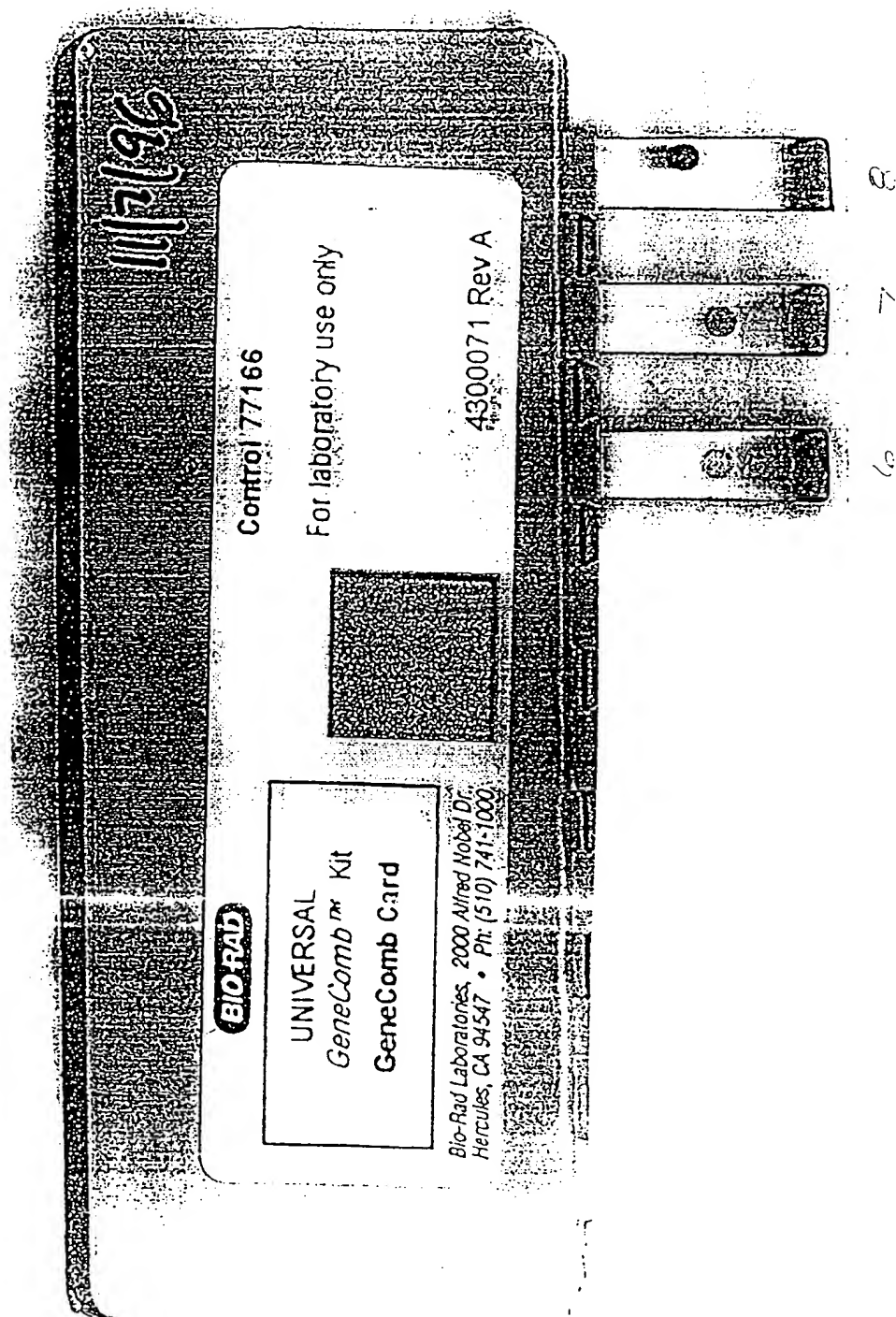


FIGURE 69

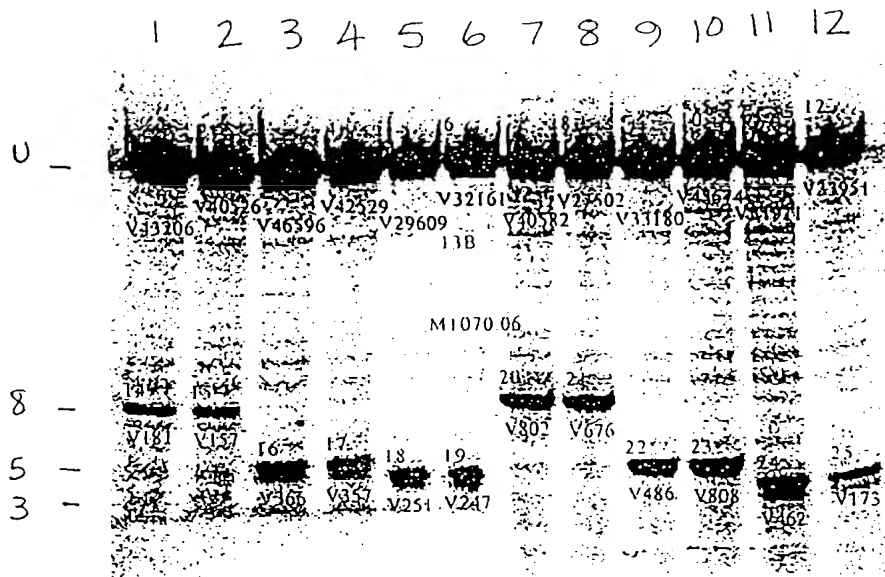


FIGURE 70

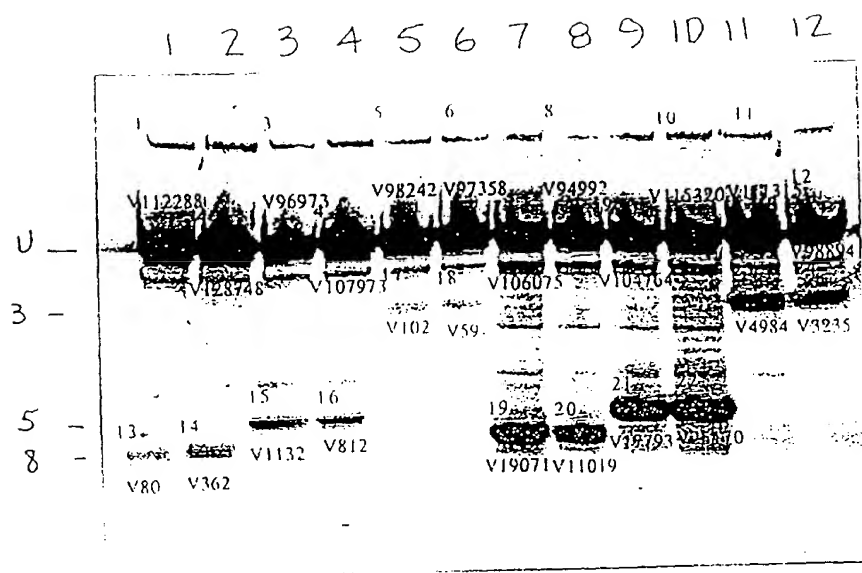
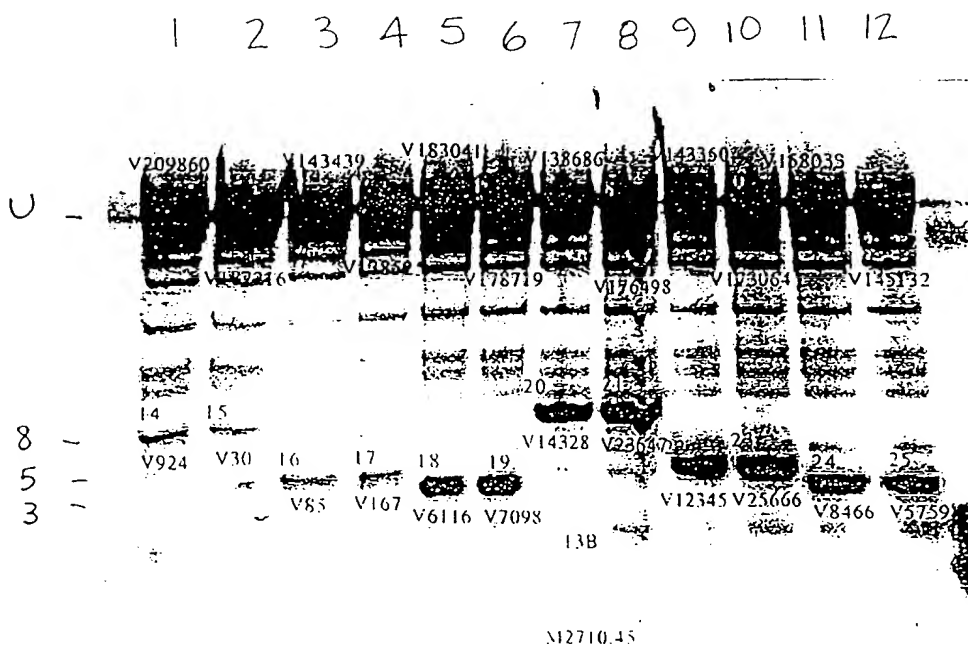


FIGURE 71



A

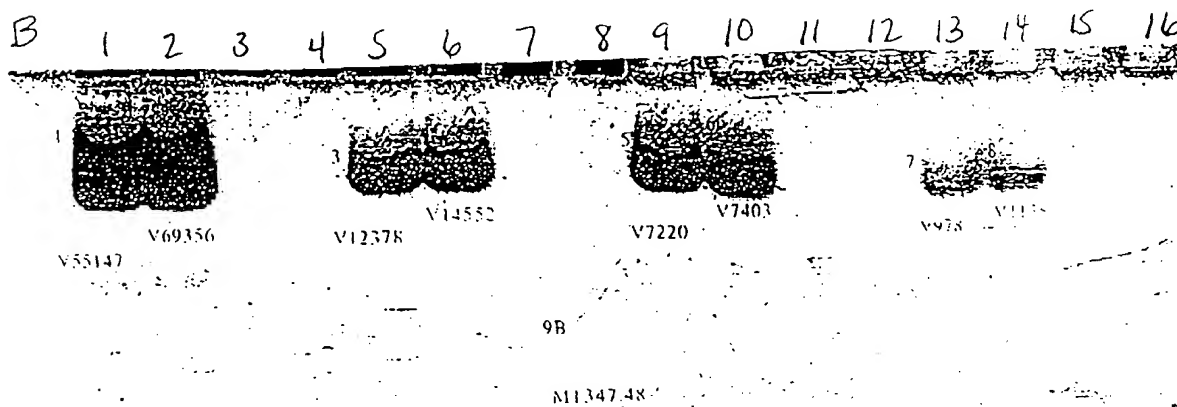
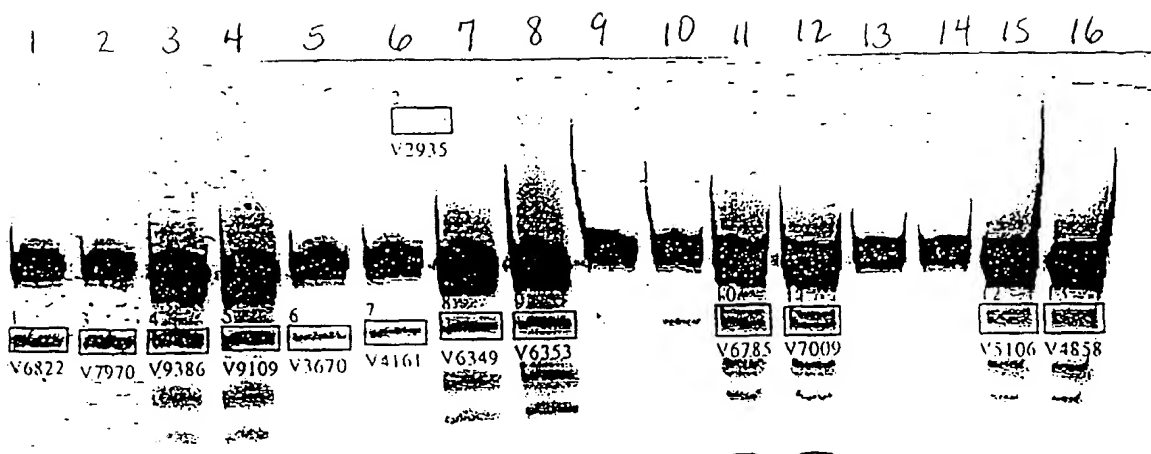
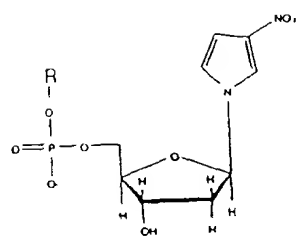


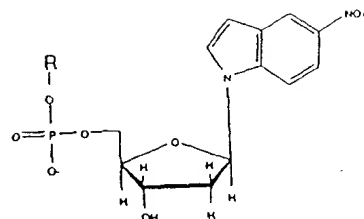
FIGURE 72



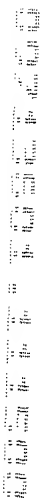
FIGURE 73



3-nitropyrrole



5-nitroindole



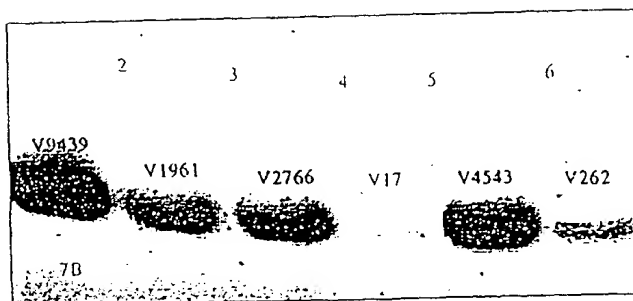
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AllComp	1Base Mismatch	AllComp	1Base Mismatch 2NI	AllComp	1Base Mismatch 1NP
---------	-------------------	---------	--------------------------	---------	--------------------------

Inval #	67	114	115	116	112	113
------------	----	-----	-----	-----	-----	-----

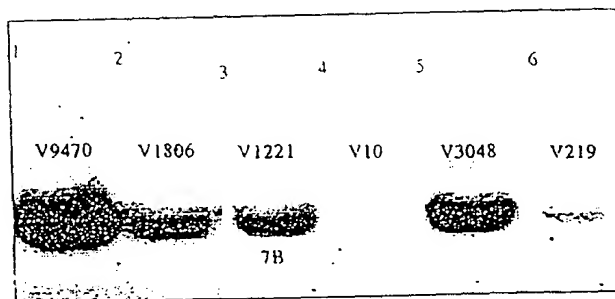
A

52°C



B

55°C



C

58°C

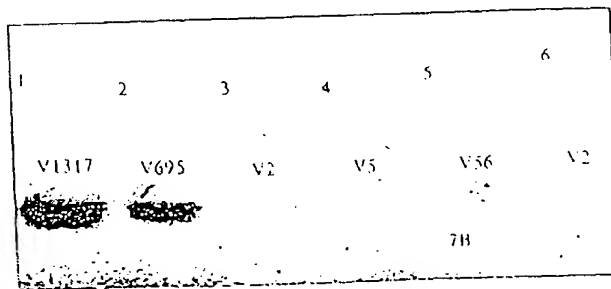
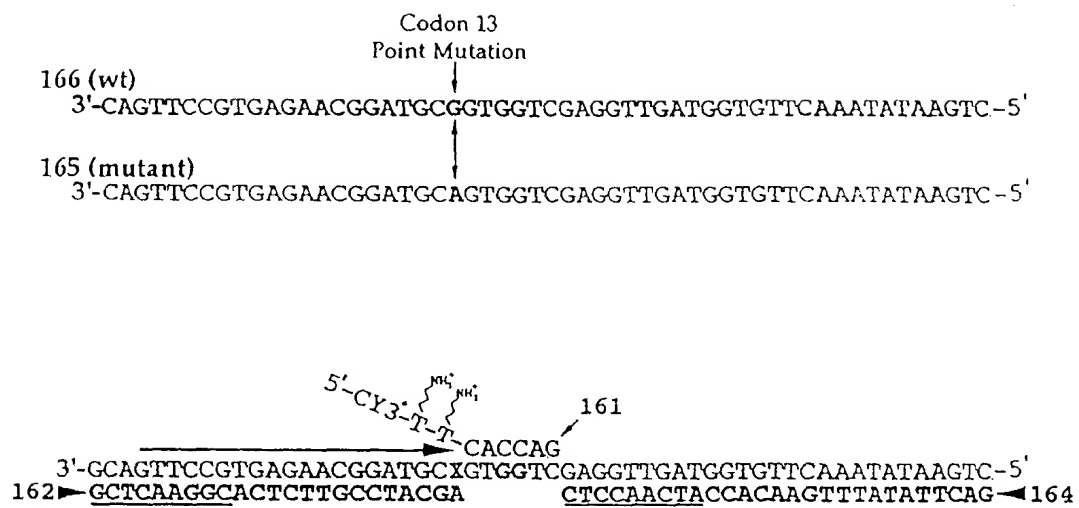


FIGURE 75

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# FIGURE 76

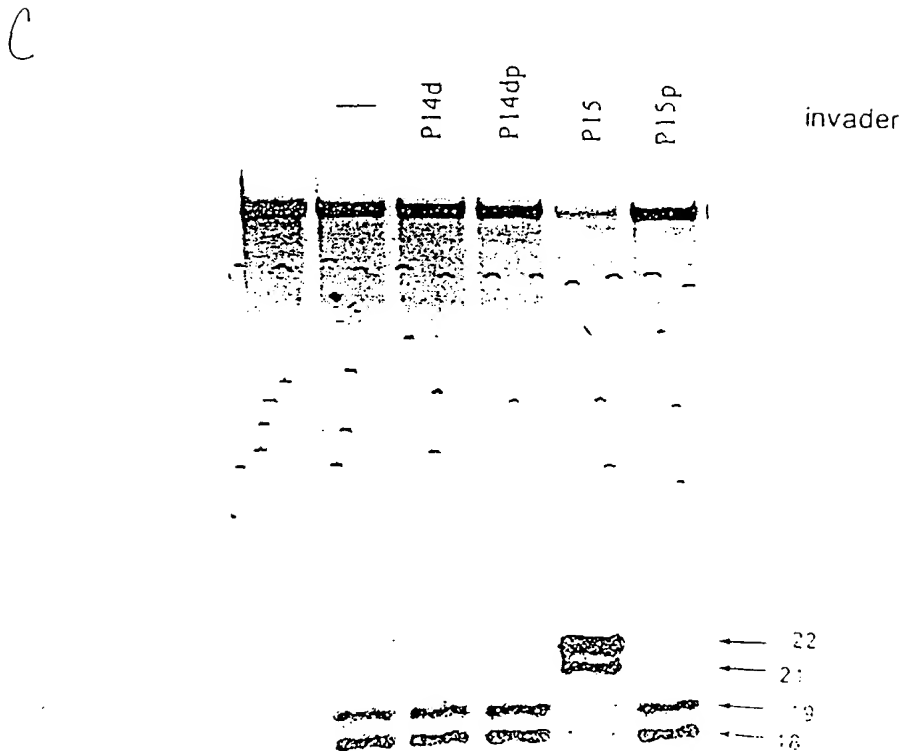


# FIGURE 77

Temp	→	47°		50°		53°		56°
Target	→	165	166	165	166	165	166	165 166



**FIGURE 78**



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# Invader 3'-end Substituents

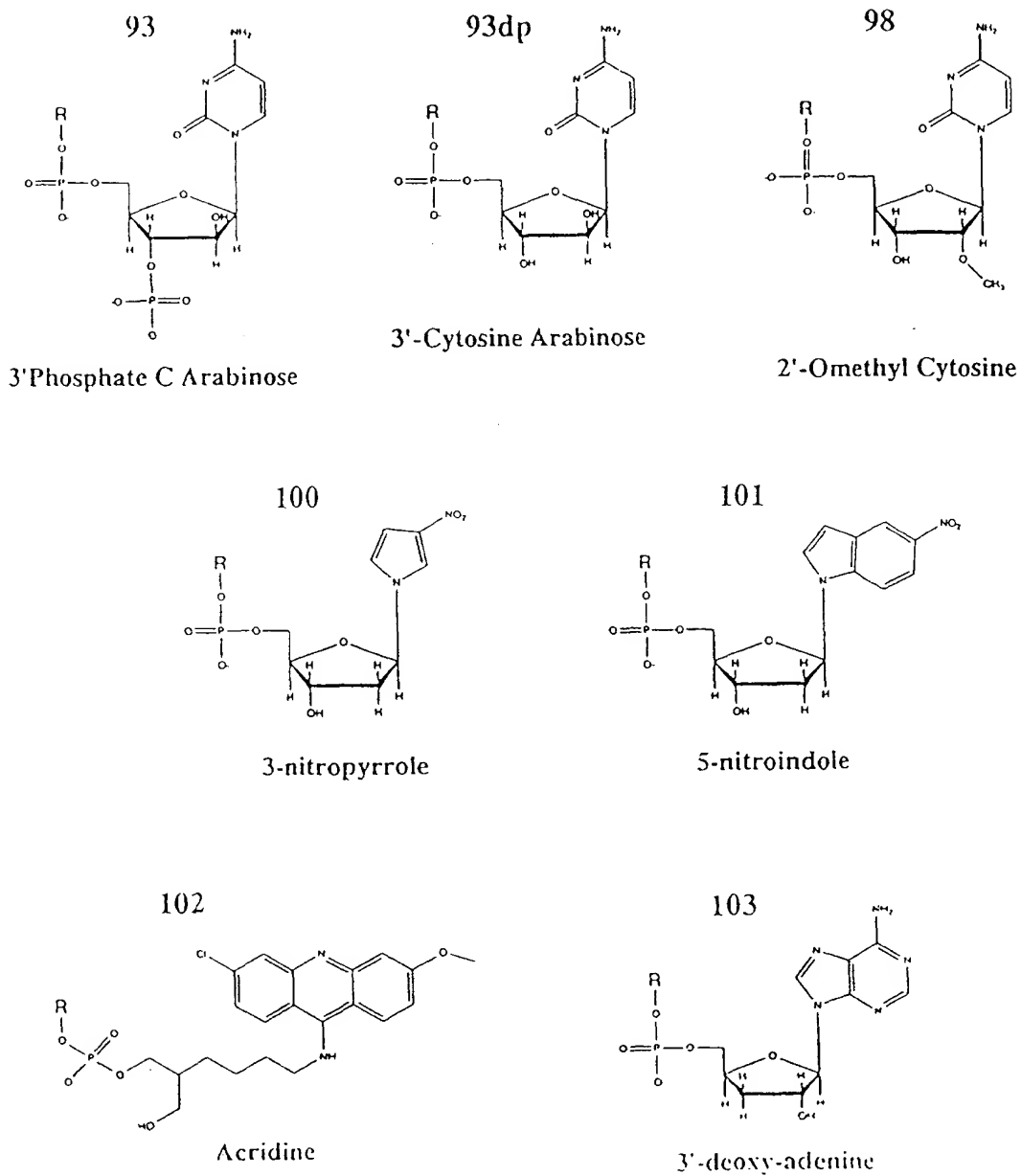


FIGURE 79

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Concentration of Probe w/ and w/o Stacker vs Temp

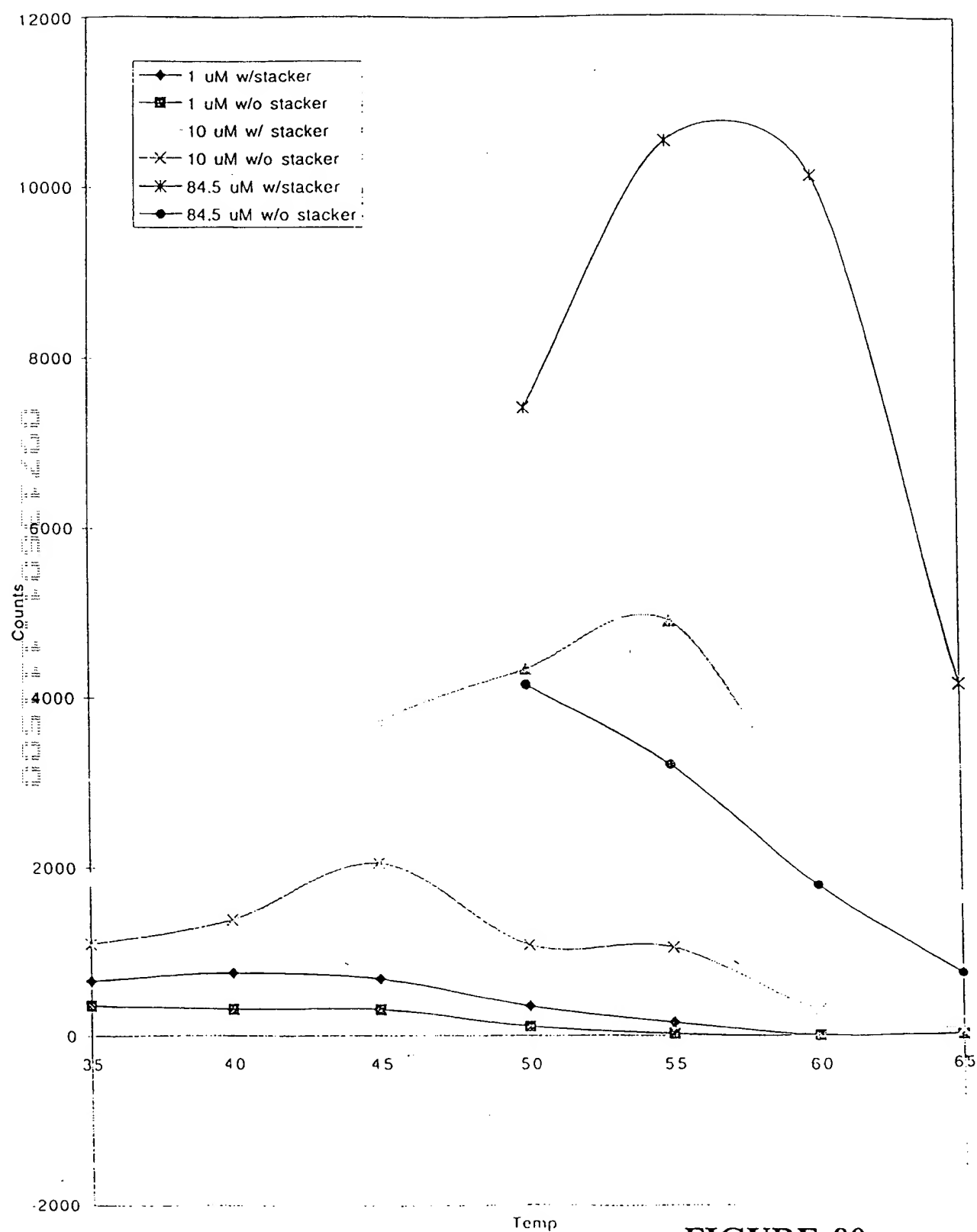


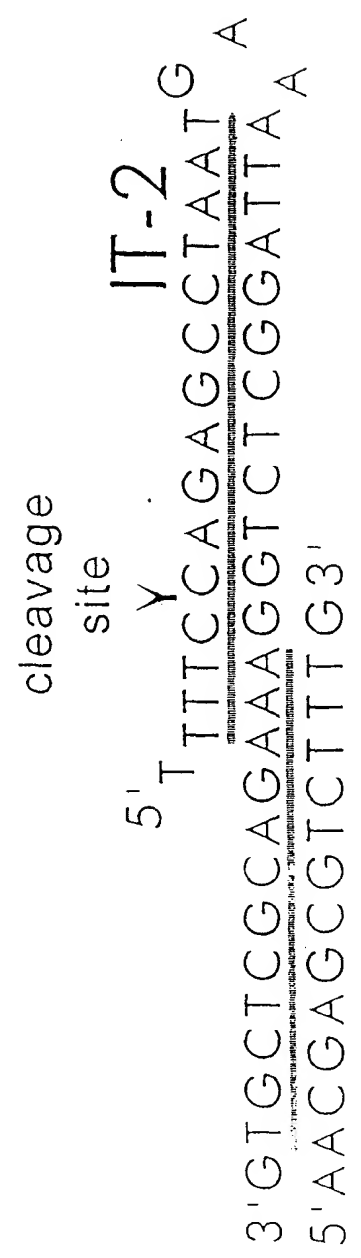
FIGURE 80

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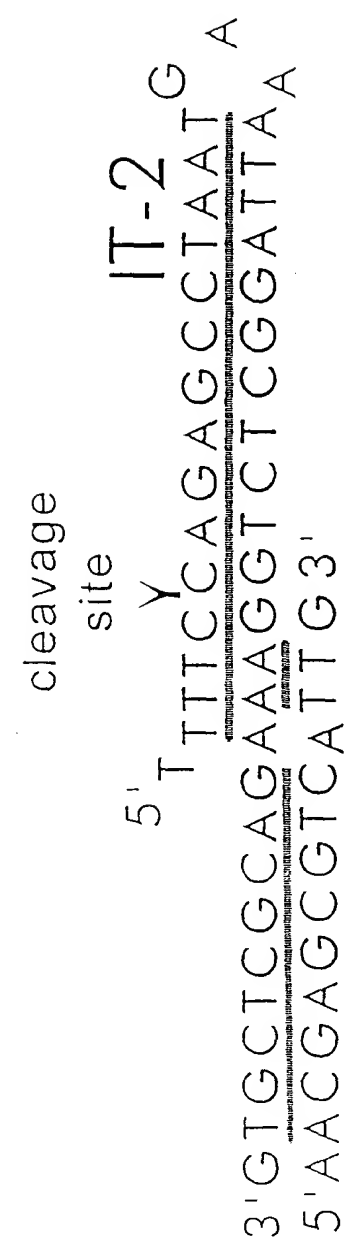


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FIGURE 81



IT-1



IT-1A4

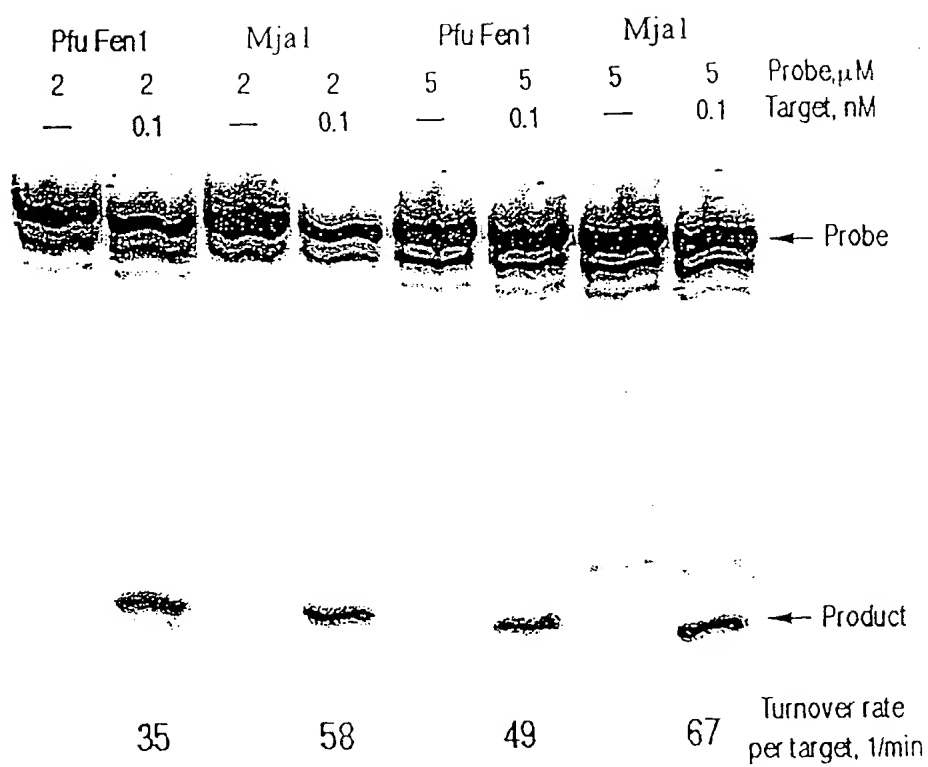
# FIGURE 82

1 2 3 4



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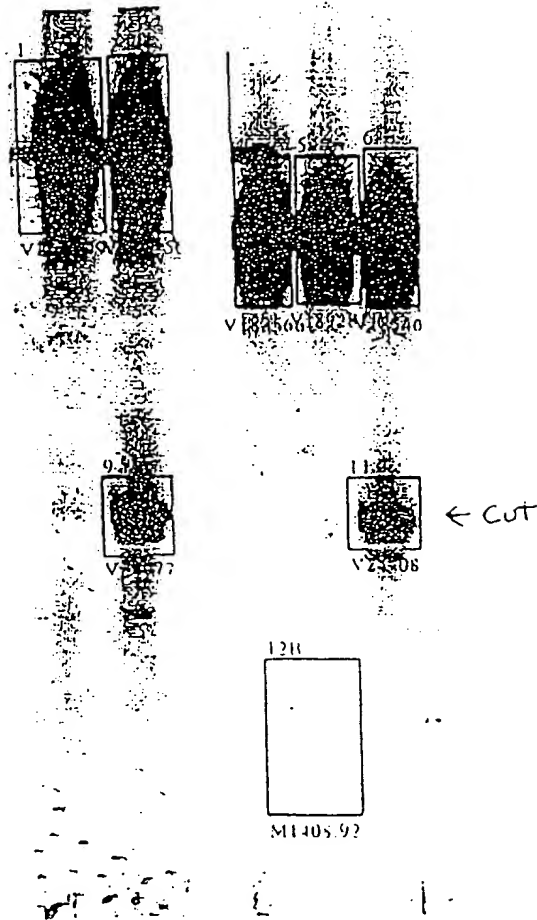
FIGURE 83



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FIGURE 84

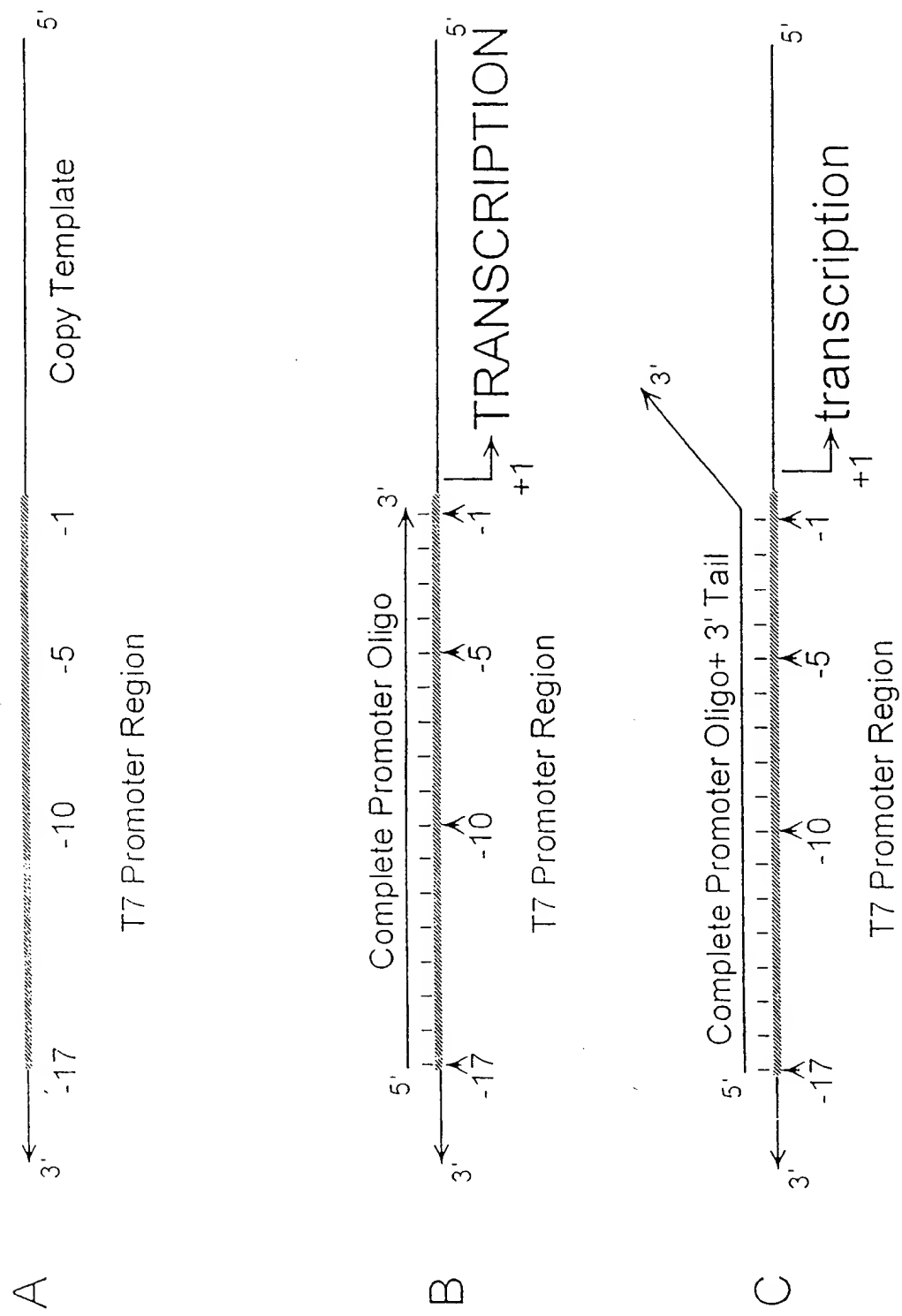
1 2 3 4 5



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FIGURE 85



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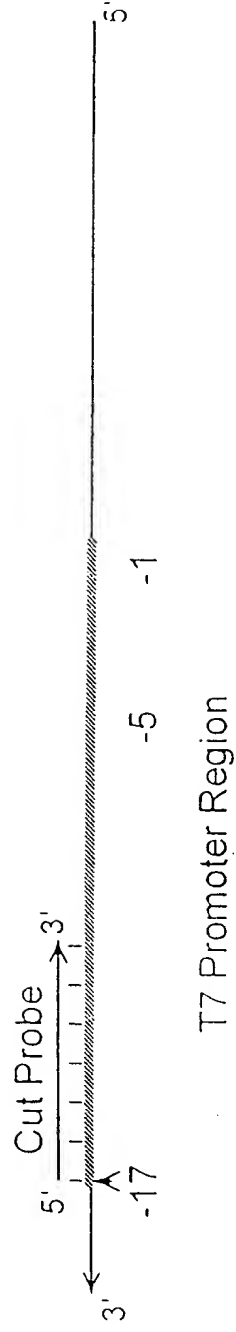


FIGURE 86A

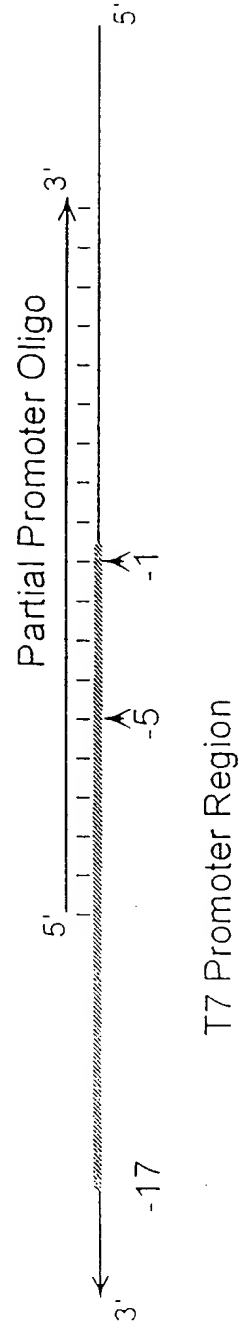


FIGURE 86B

FIGURE 86C

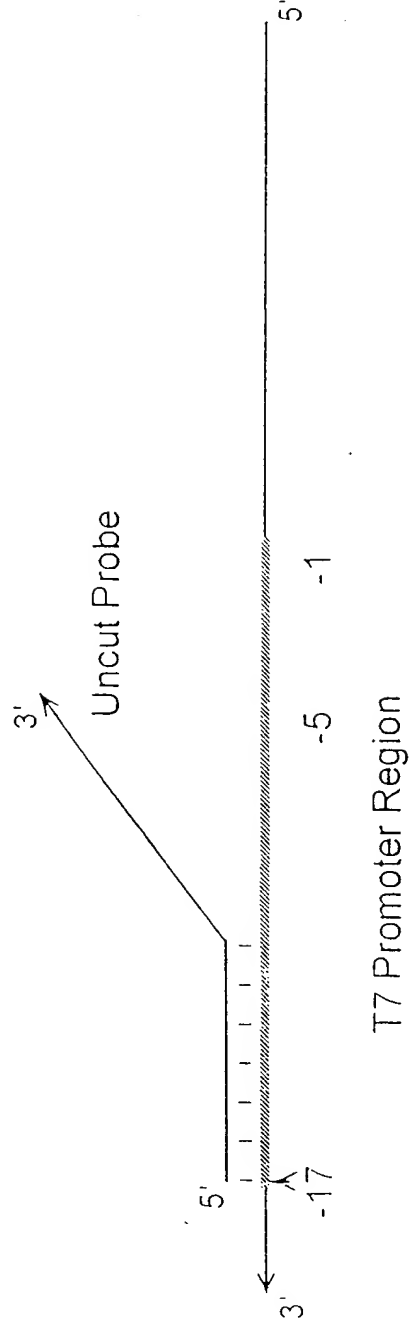
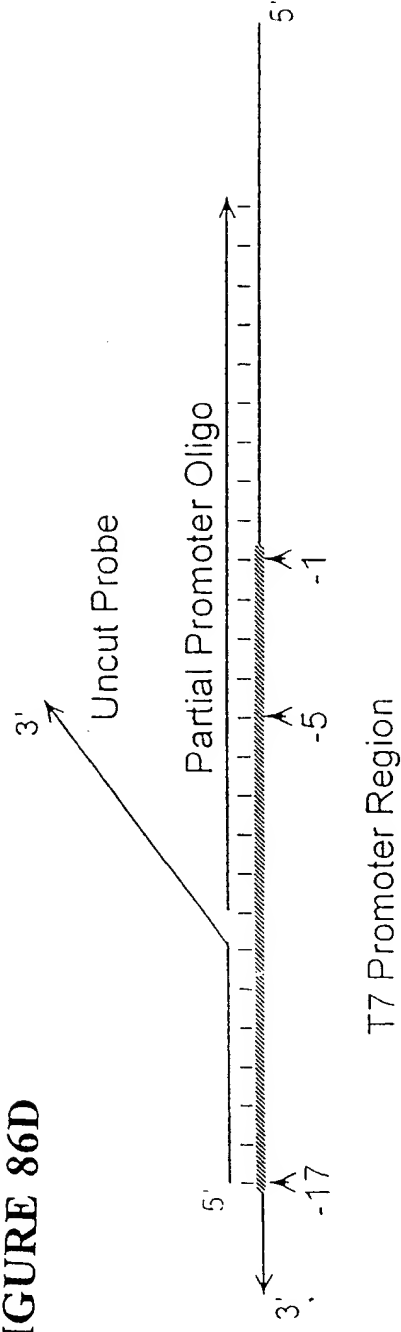
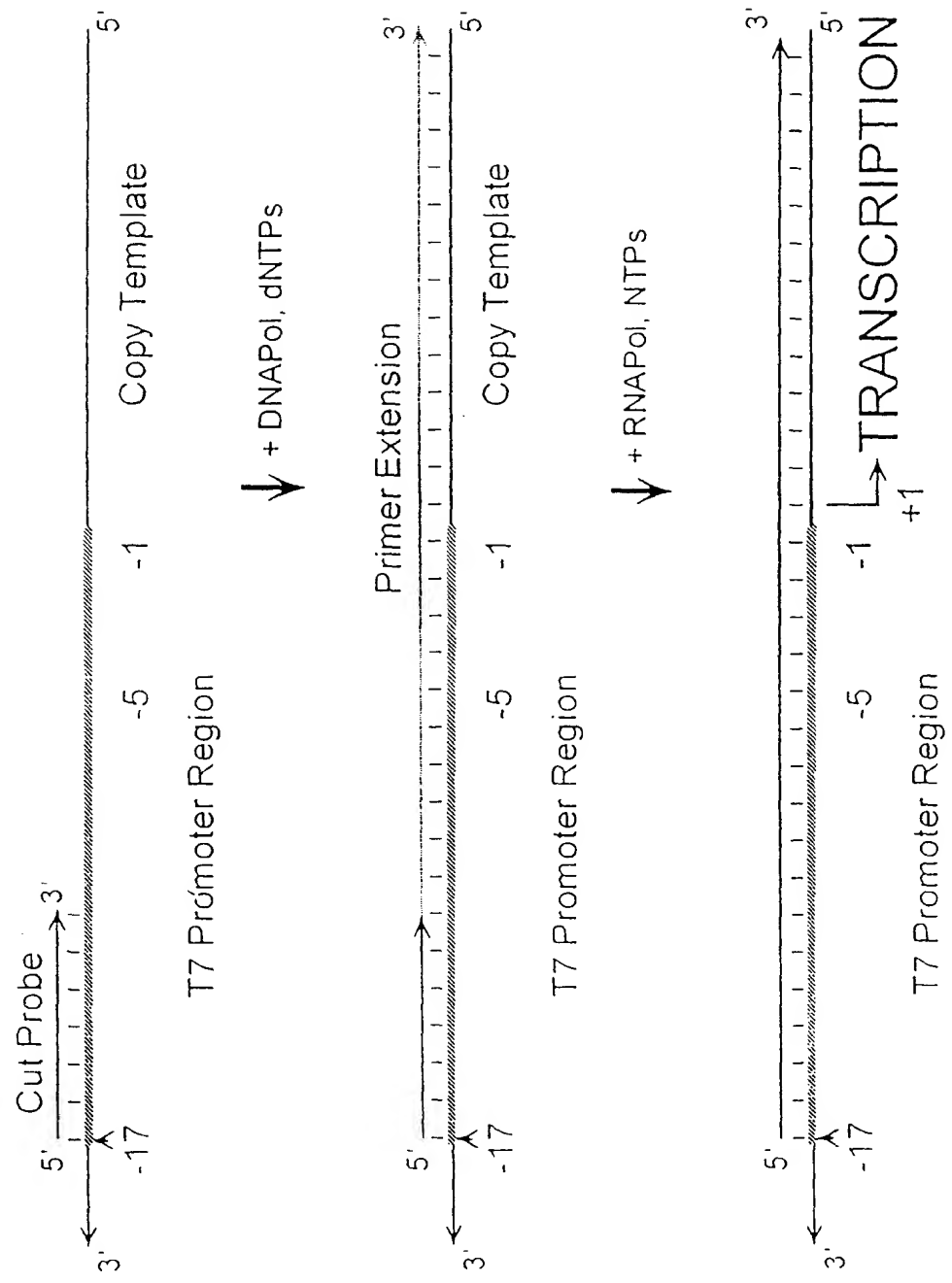


FIGURE 86D



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FIGURE 87





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FIGURE 88A

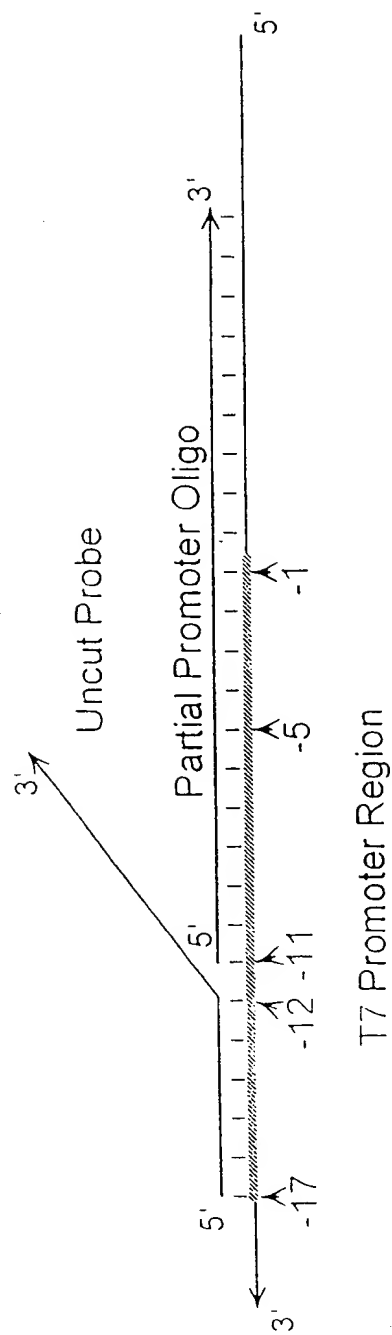


FIGURE 88B

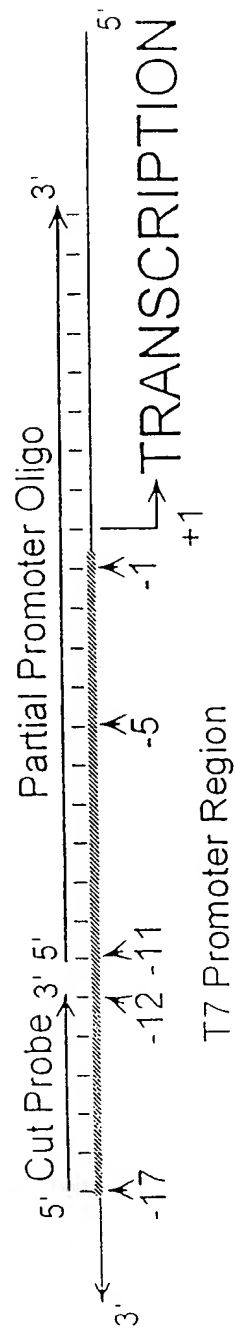
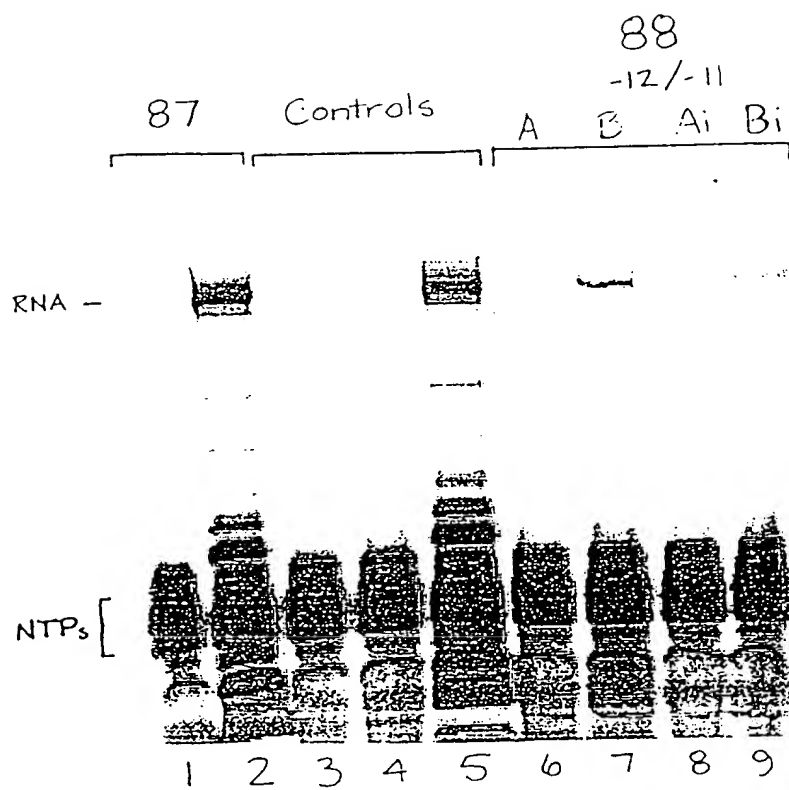


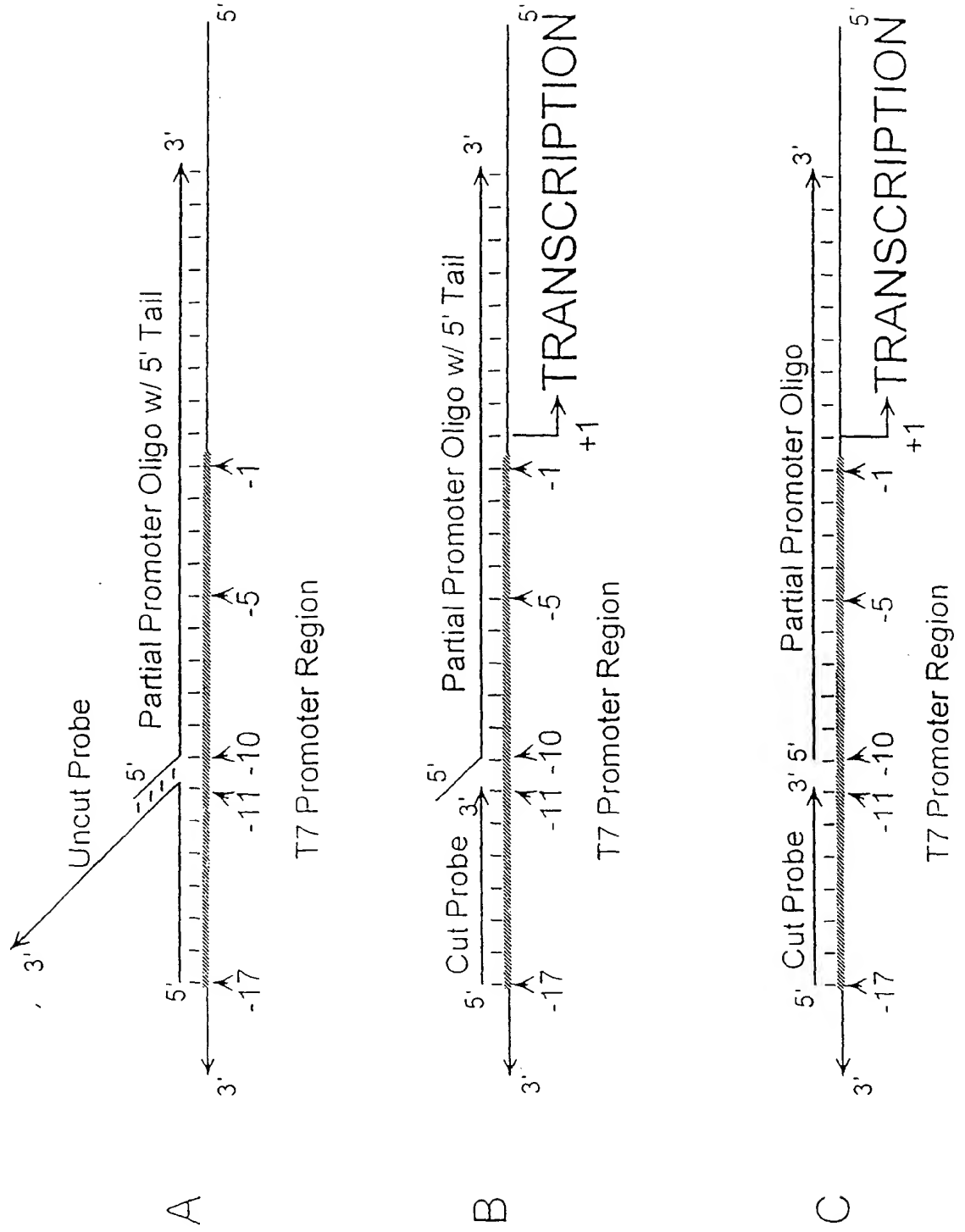
FIGURE 89



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FIGURE 90



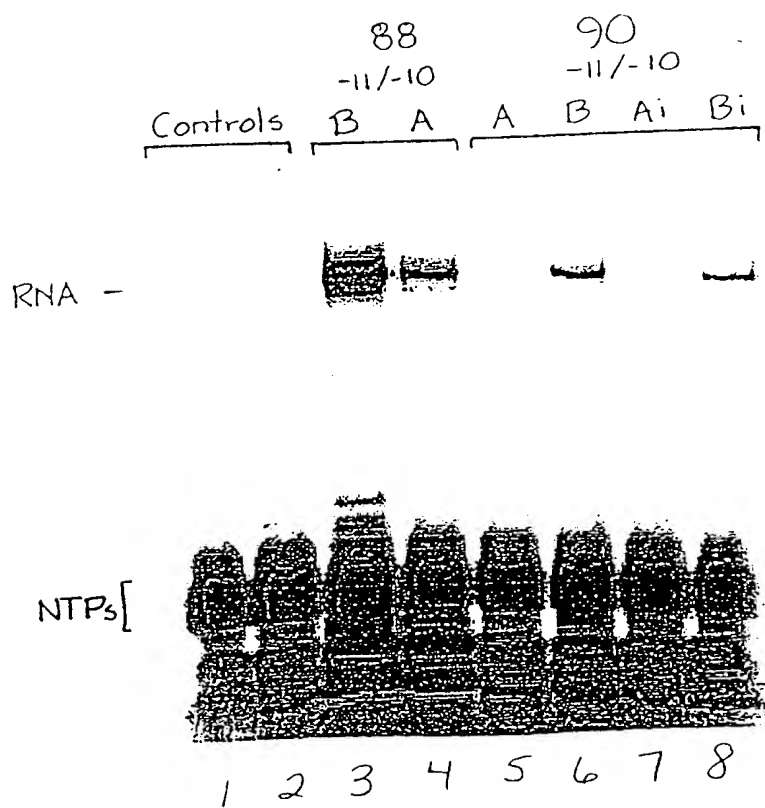
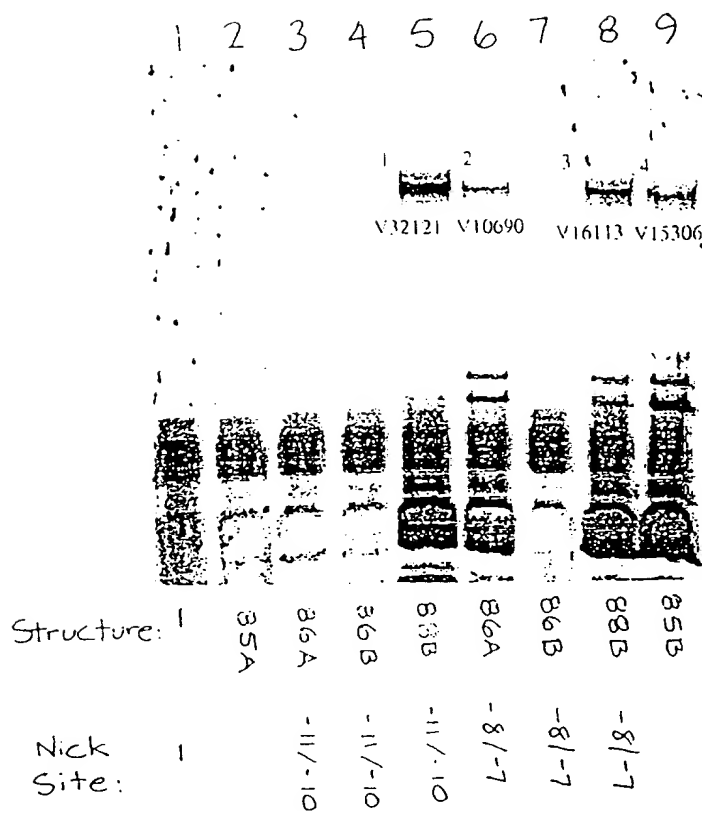


FIGURE 91

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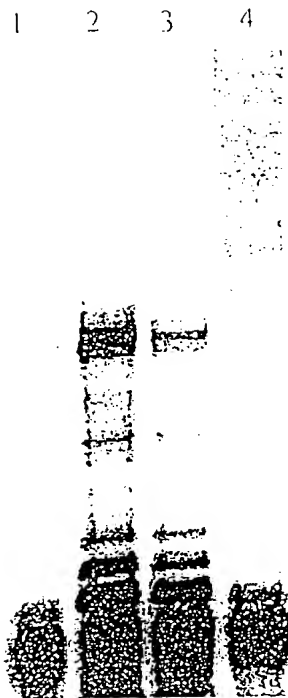
FIGURE 92



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FIGURE 93

RNA —



1  
3'-gctttaattatgctgagtqatatcccagaagataacctccagttttgt-5'  
-23 -20 -15 -10 -5 -1  
| T7 promoter region |

85A

2  
5'-cgaaattaatacgaactcactata-3'  
3'-gctttaattatgctgagtqatatcccagaagataacctccagttttgt-5'  
-23 -20 -15 -10 -5 -1  
| T7 promoter region |

85B

3  
#073-065  
5'-cgaaattaatacgaactcactatacccagaa-3'  
3'-gctttaattatgctgagtqatatcccagaagataacctccagttttgt-5'  
-23 -20 -15 -10 -5 -1  
| T7 promoter region |

85C

4 No DNA

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5' Partial Promoter 3' 5' Cut Probe 3'

FIGURE 94

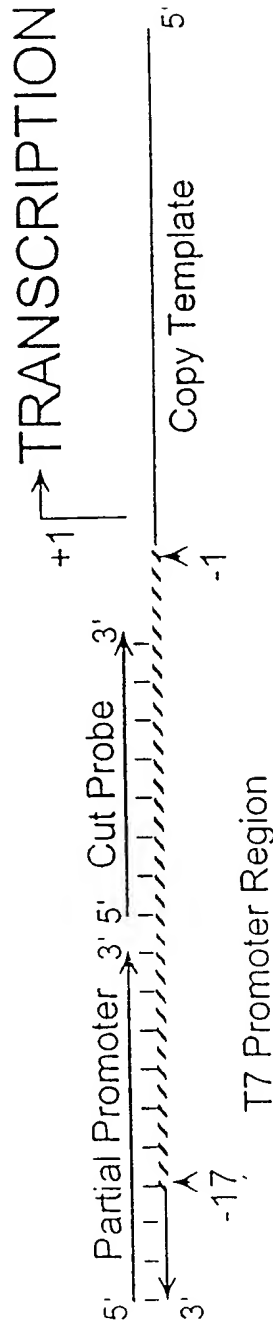


FIGURE 95A

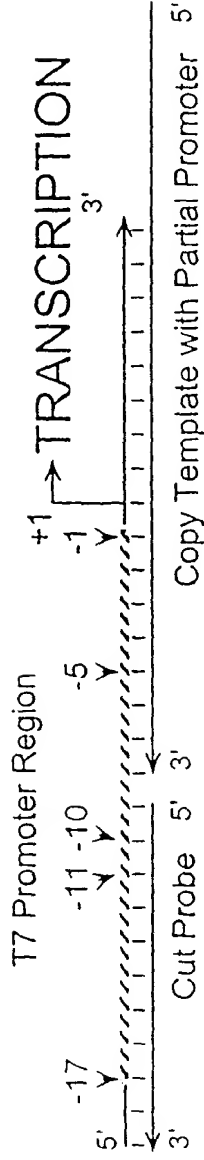


FIGURE 95B

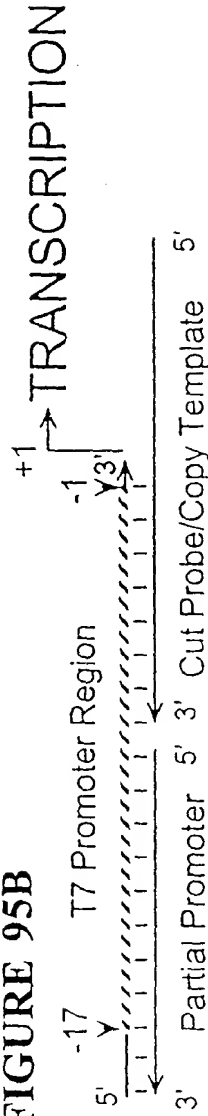


FIGURE 95C

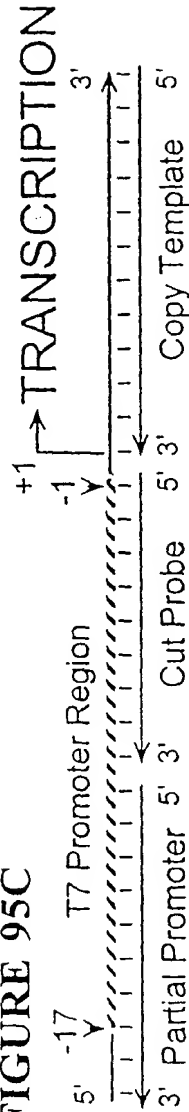


FIGURE 95D

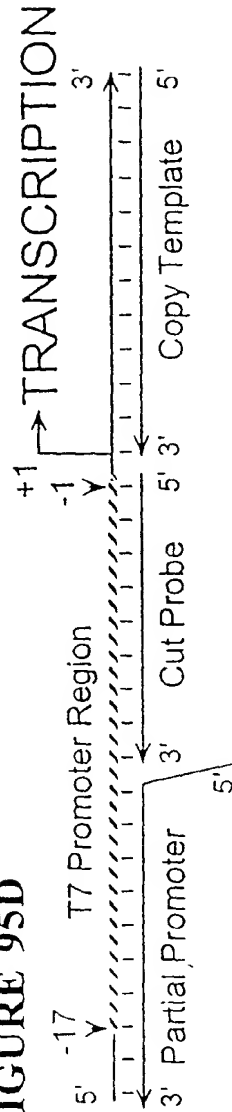
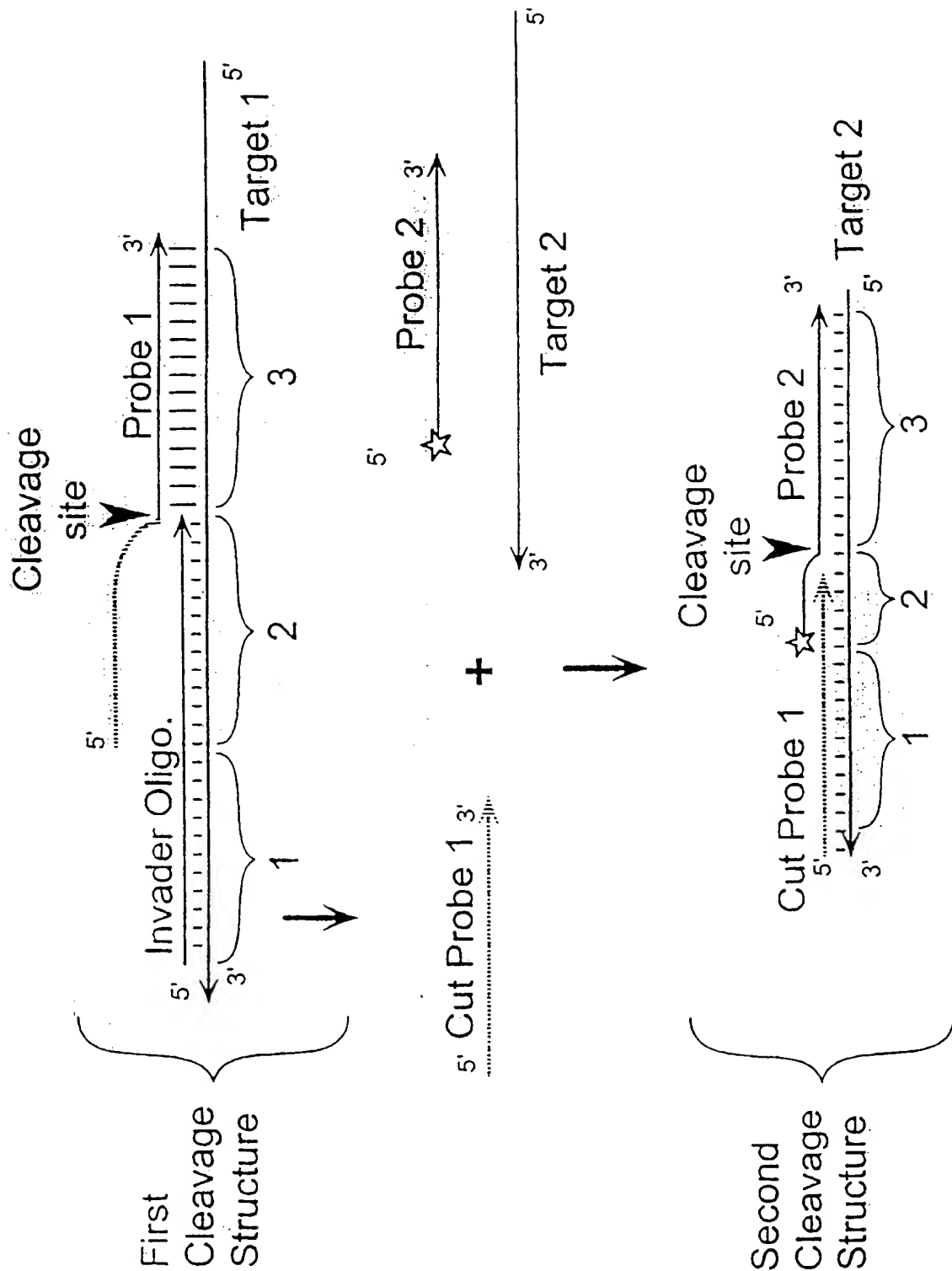




FIGURE 96



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FIGURE 97

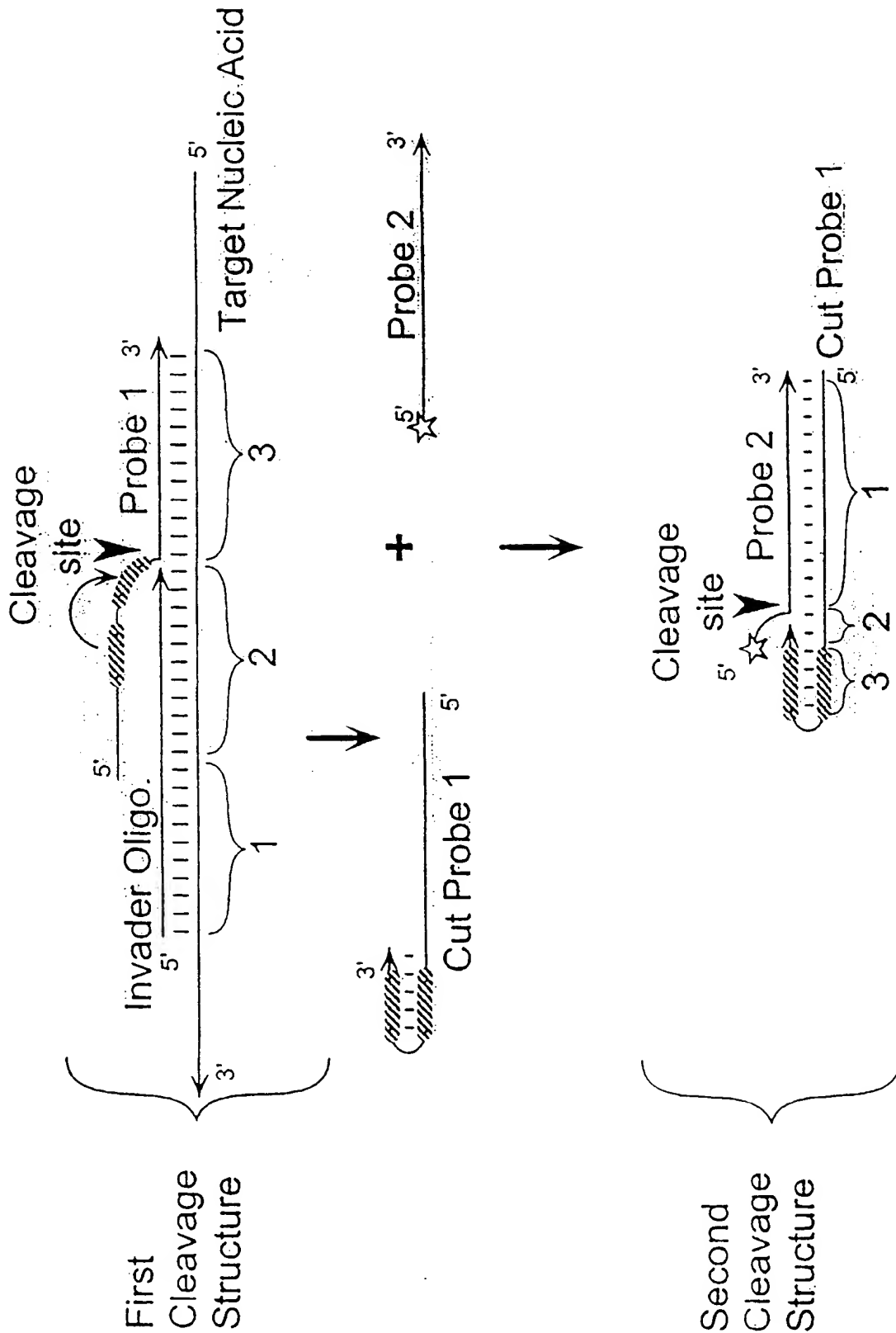


FIGURE 98

PR1 probe

Cleavage site

5'FITTTCAGAGCCTAAT<sup>G3'</sup>

IT3 Invader-Target

A<sup>A</sup>ACGAGCGTCTTT<sup>G3'</sup>  
G TGCTCGCAGAAAGGTCTCGGATTAATTTTTTTTT5'

IT3-8 Invader-Target

A<sup>A</sup>AGCGTCTT<sup>G3'</sup>  
G TCGCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-6 Invader-Target

A<sup>A</sup>CGTCTT<sup>G3'</sup>  
G GCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-4 Invader-Target

A<sup>A</sup>TCTT<sup>G3'</sup>  
G AGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-3 Invader-Target

A<sup>A</sup>CTT<sup>G3'</sup>  
G GAAGGTCTCGGATTAATTTTTTTTT5'

IT3-0 Invader-Target

3'GAAGGTCTCGGATTAATTTTTTTTT5'

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FIGURE 99

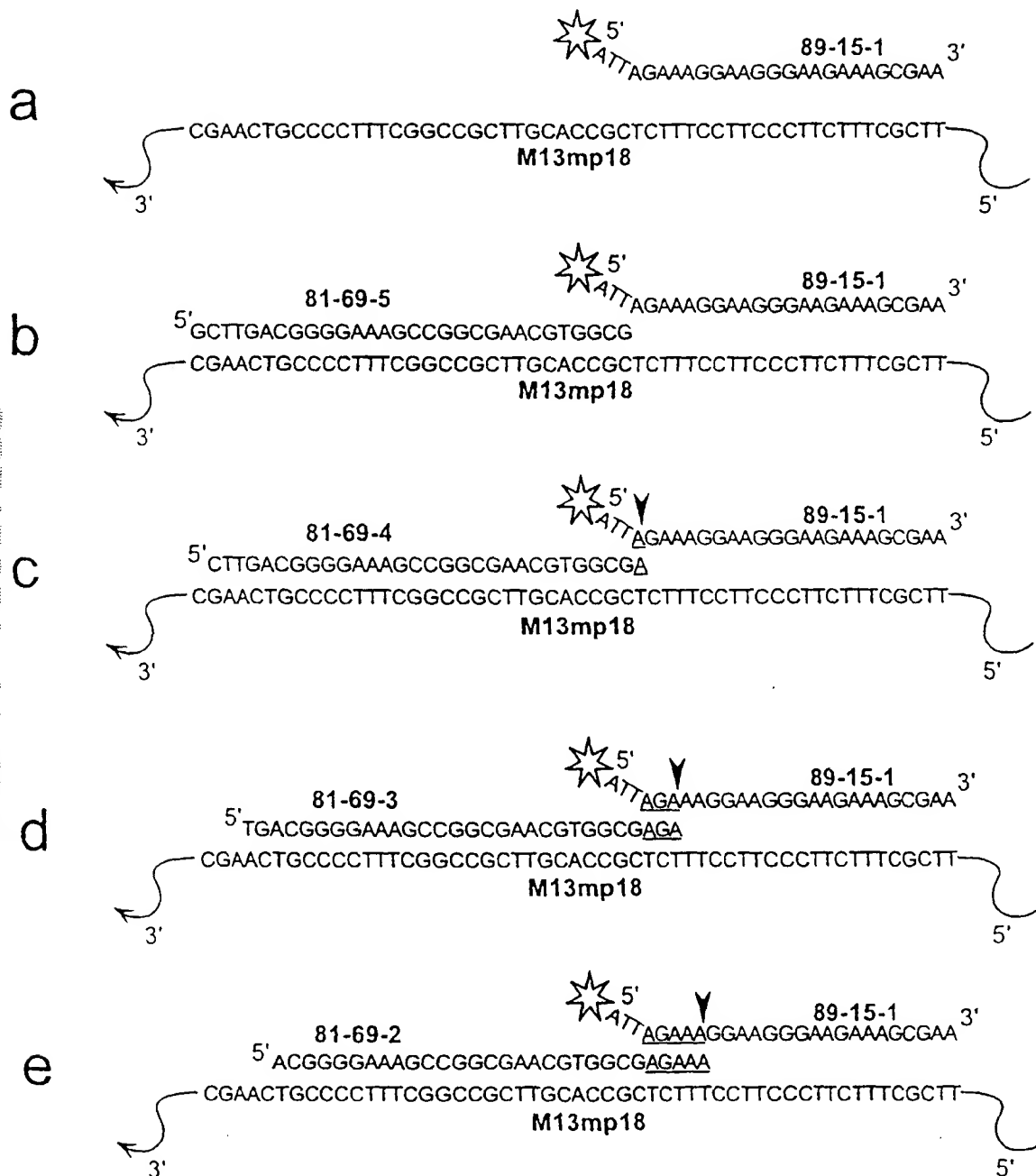
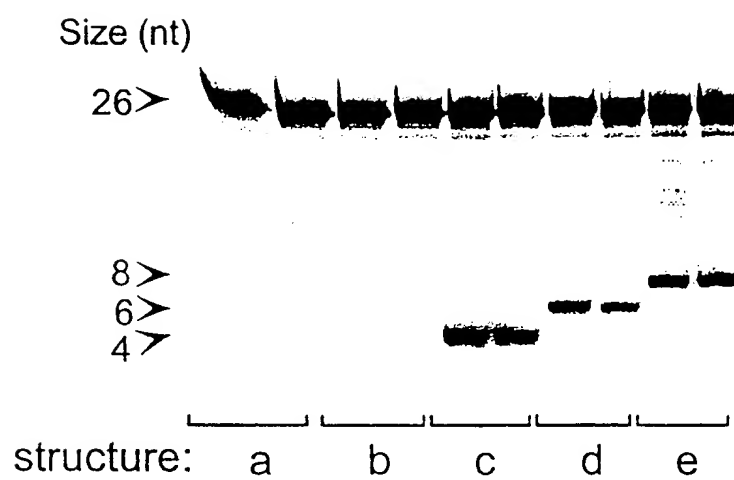


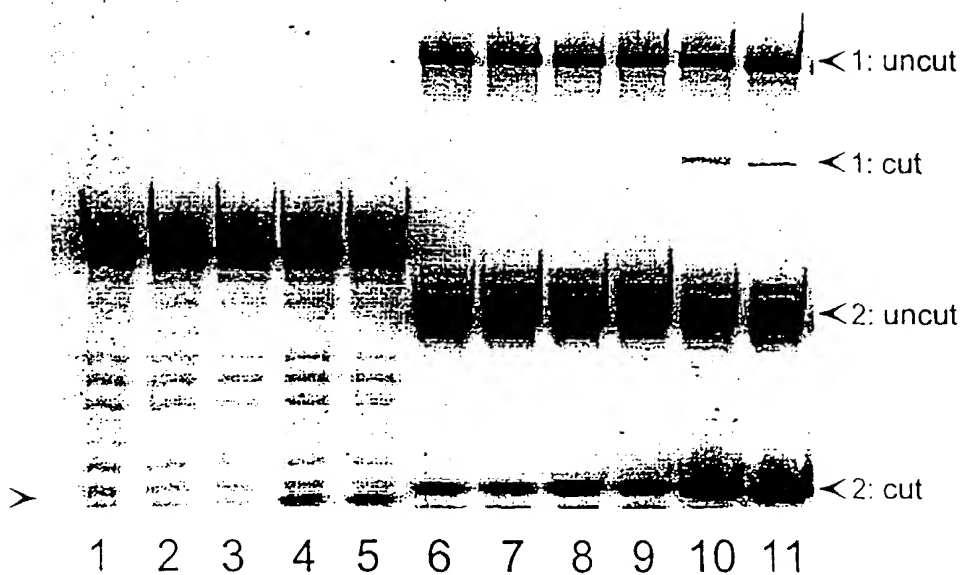
FIGURE 100



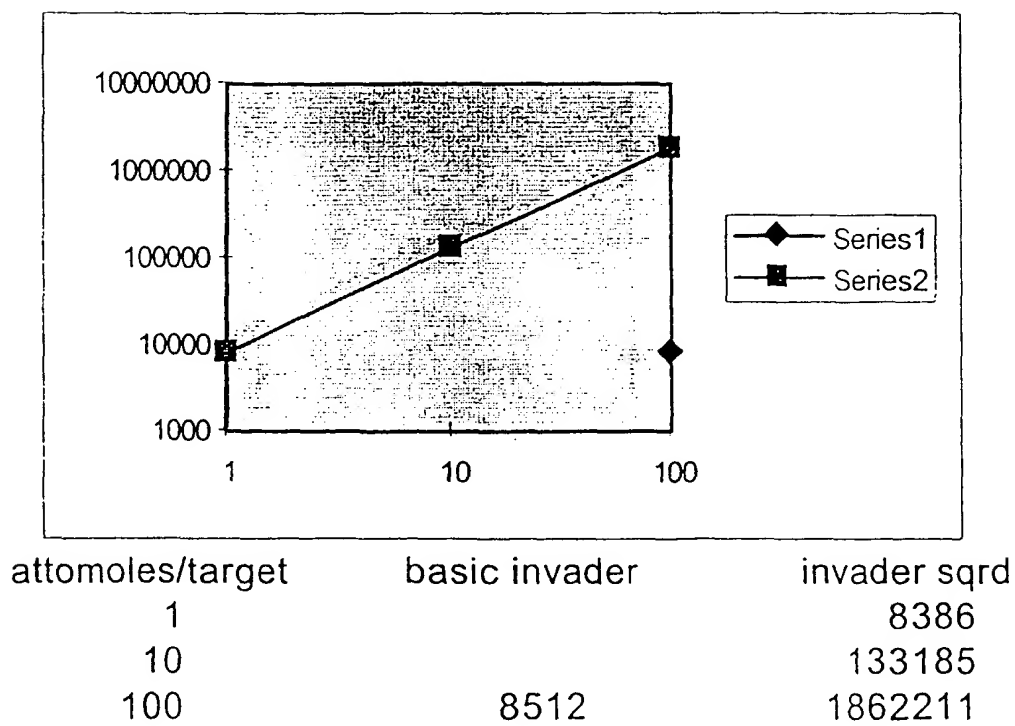
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FIGURE 101

a

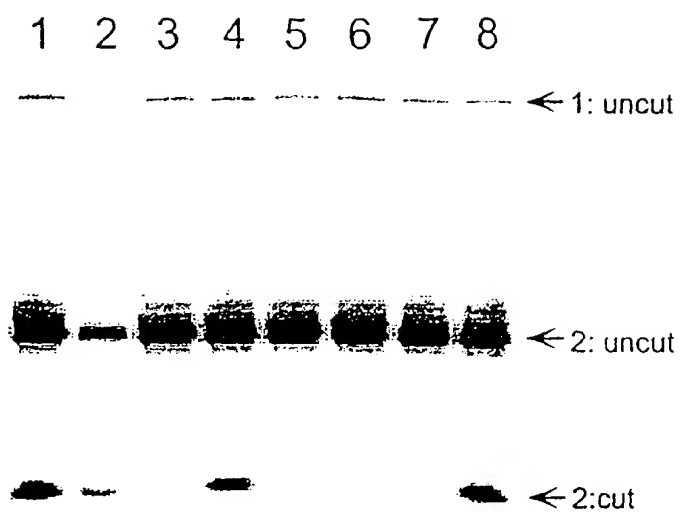


b



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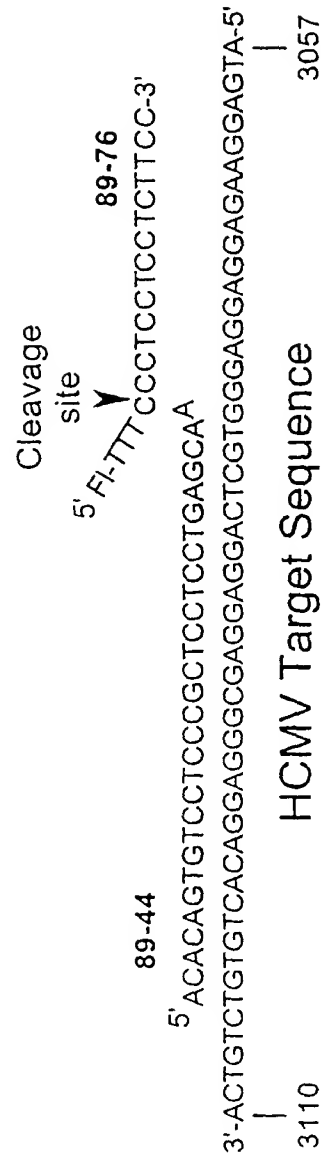
FIGURE 102



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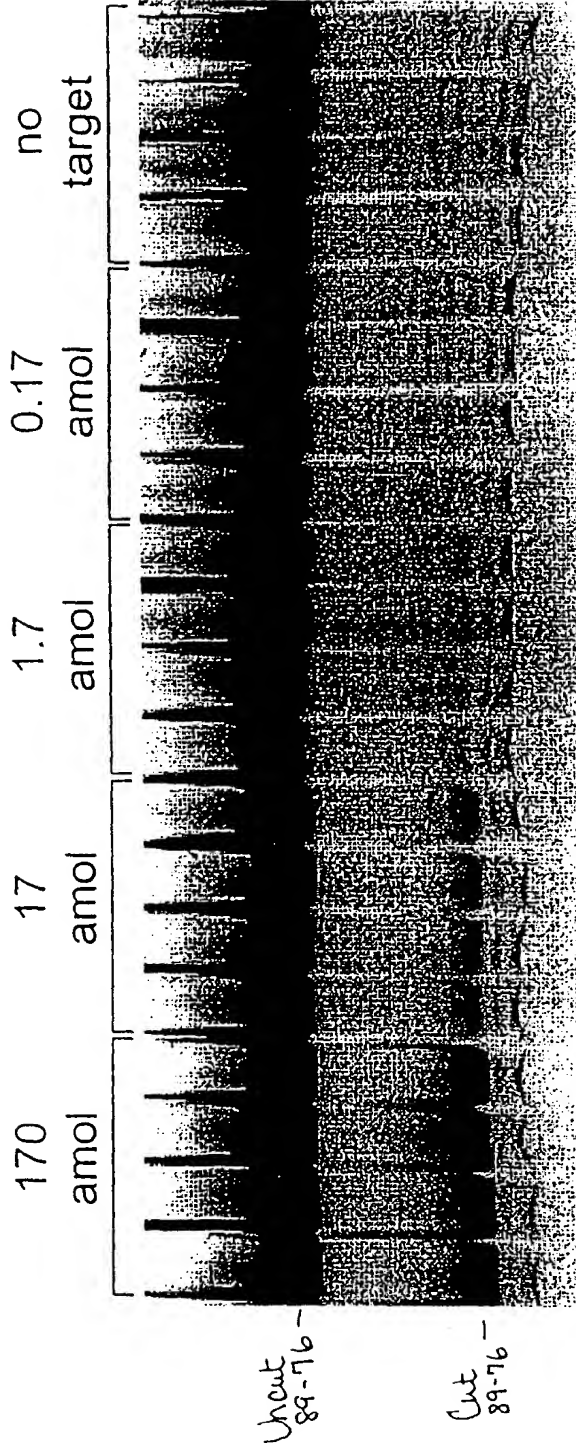
FIGURE 103





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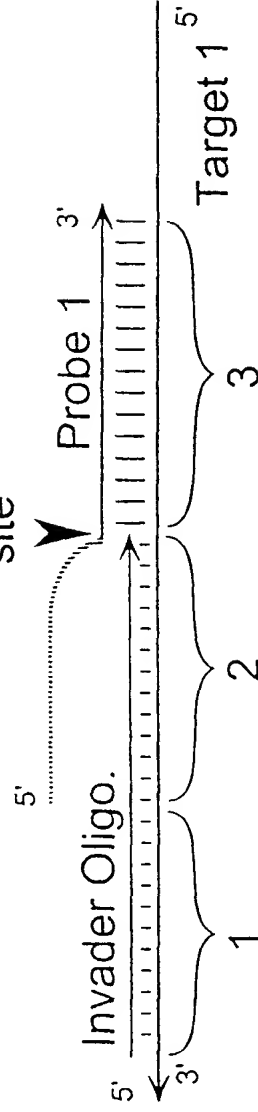
FIGURE 104



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FIGURE 105

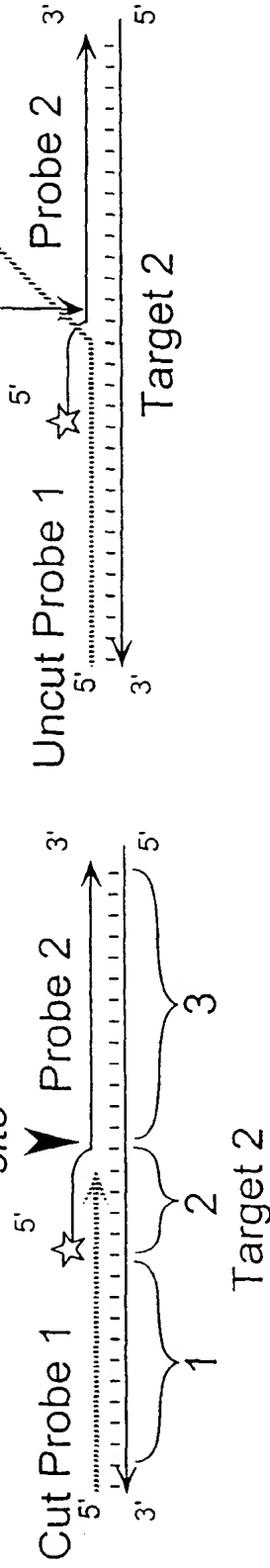
Cleavage site



1

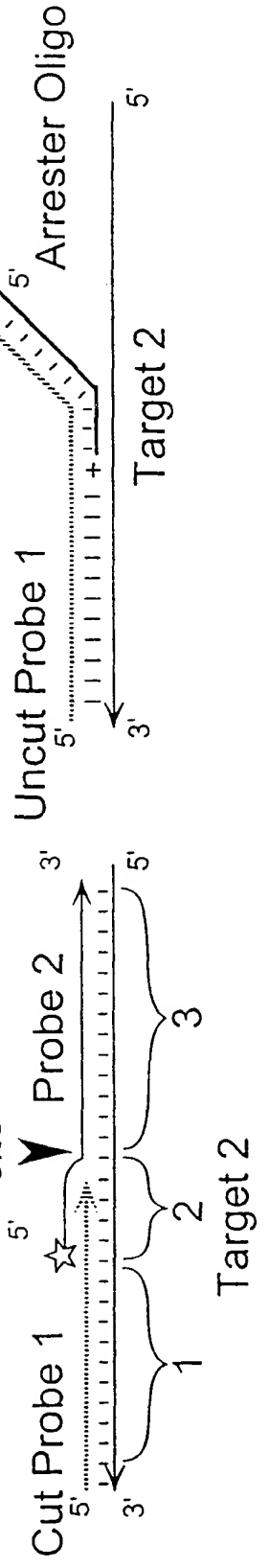
Background cleavage site

Cleavage site



2a

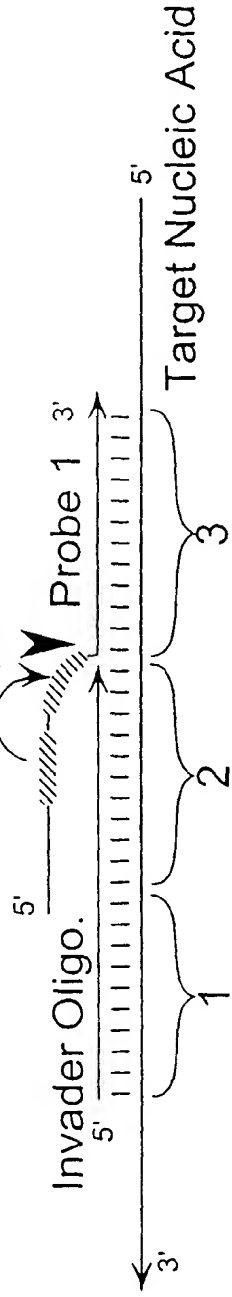
Cleavage site



2b

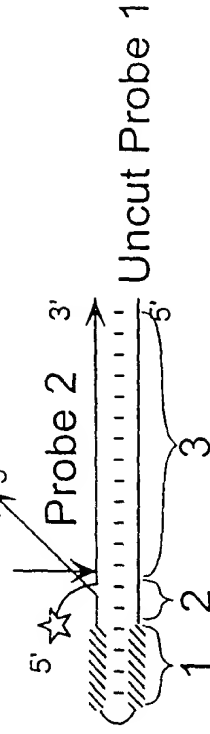
FIGURE 106

Cleavage site



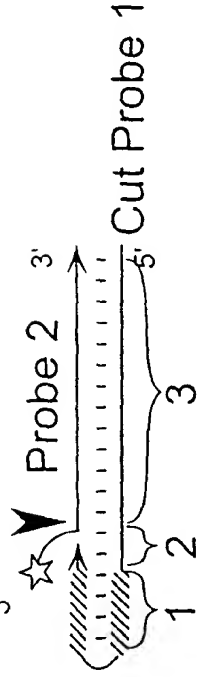
1

Background cleavage site

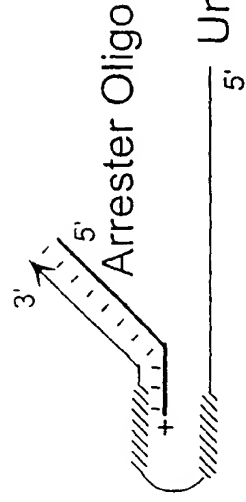


2a

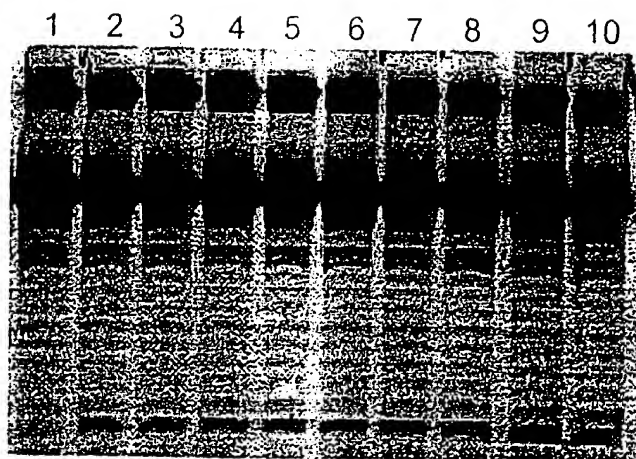
Cleavage site



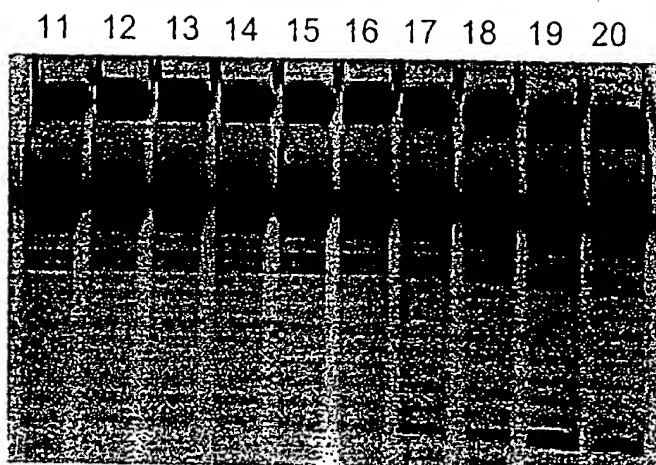
2b



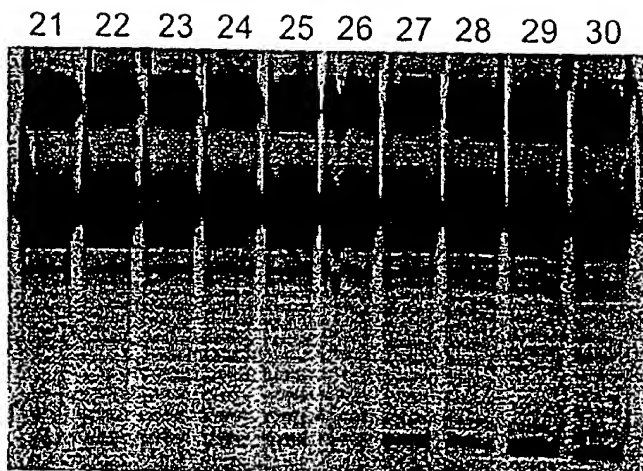
A



B



C

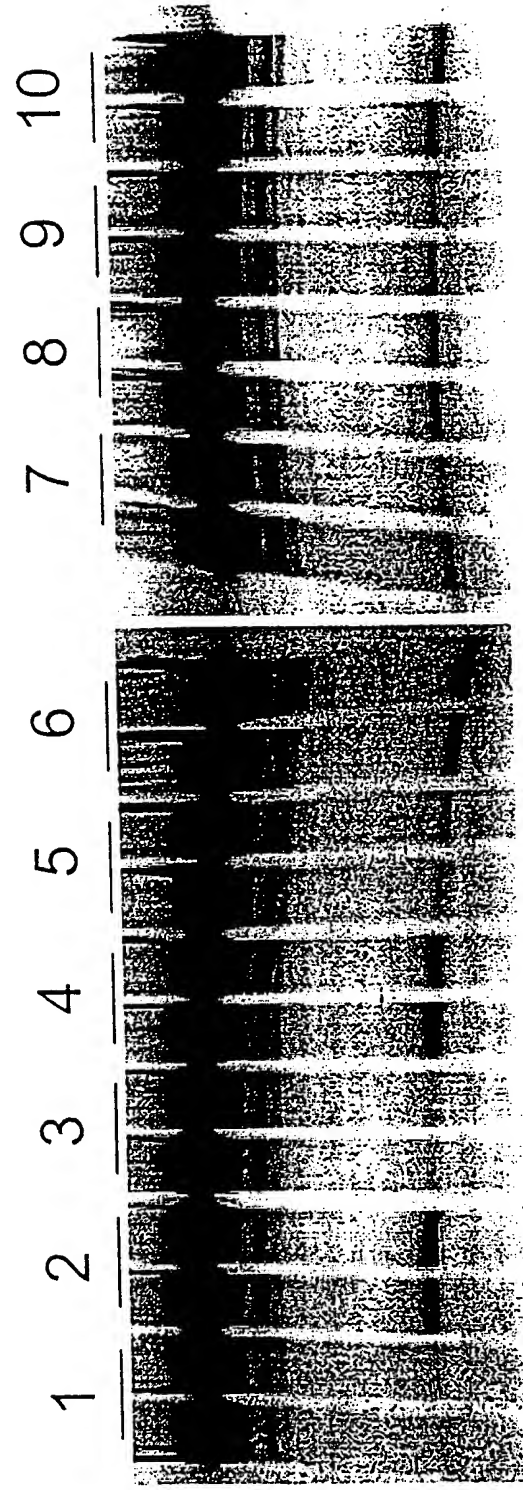


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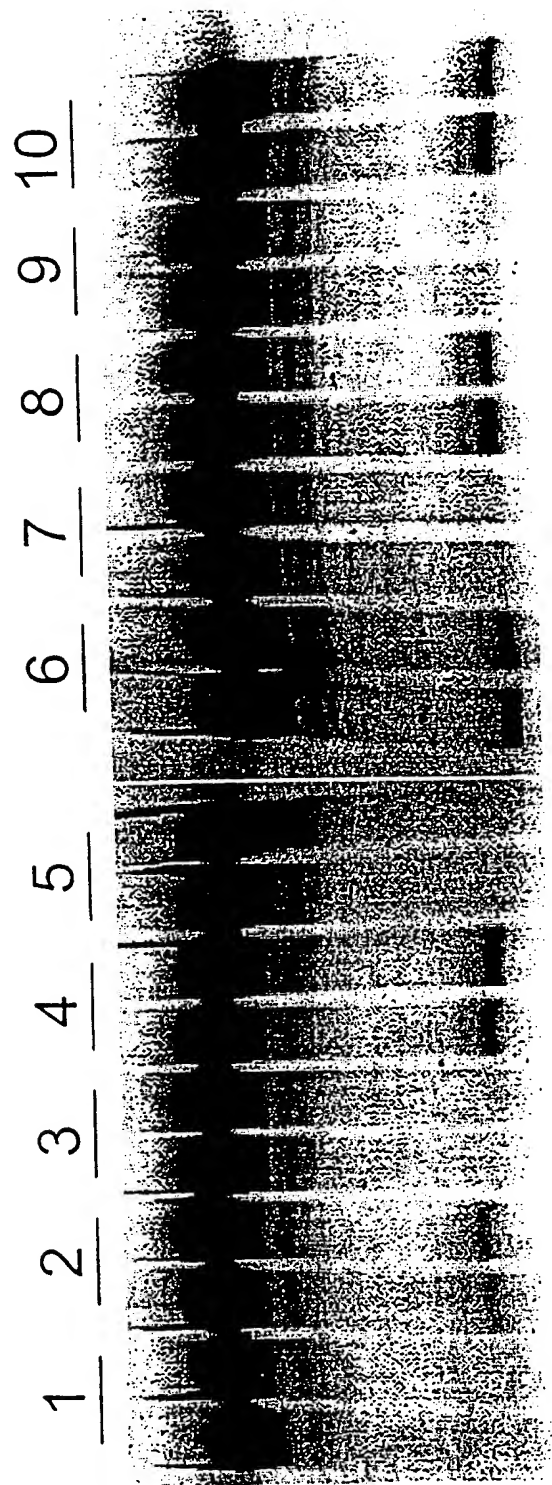
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FIGURE 108A



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FIGURE 108B



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FIGURE 108C

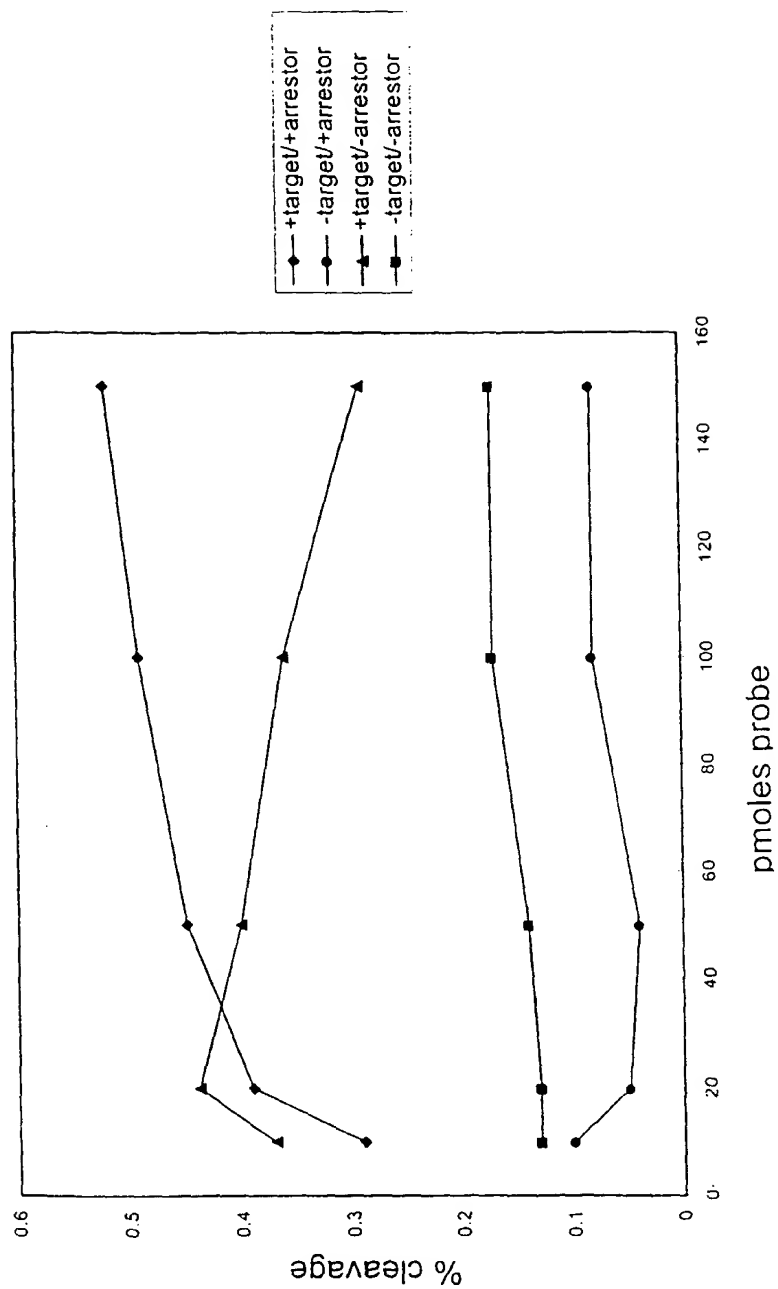
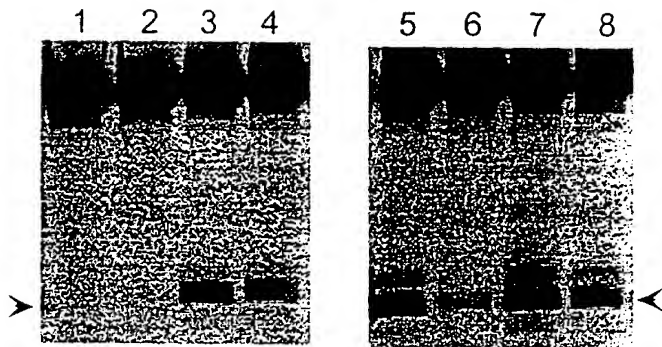


FIGURE 109A



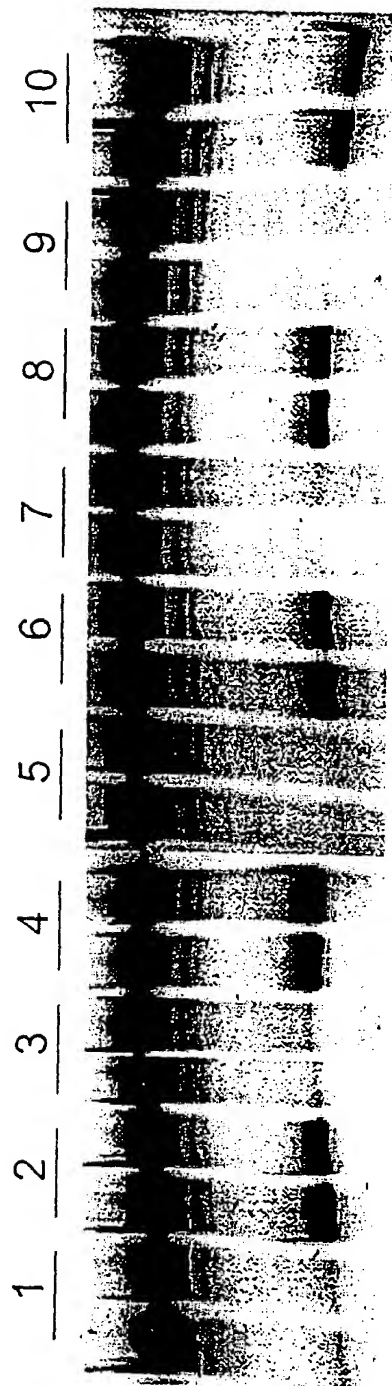
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QCTT-TEST-00

FIGURE 110A



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DEPT. OF DEFENSE

FIGURE 110B

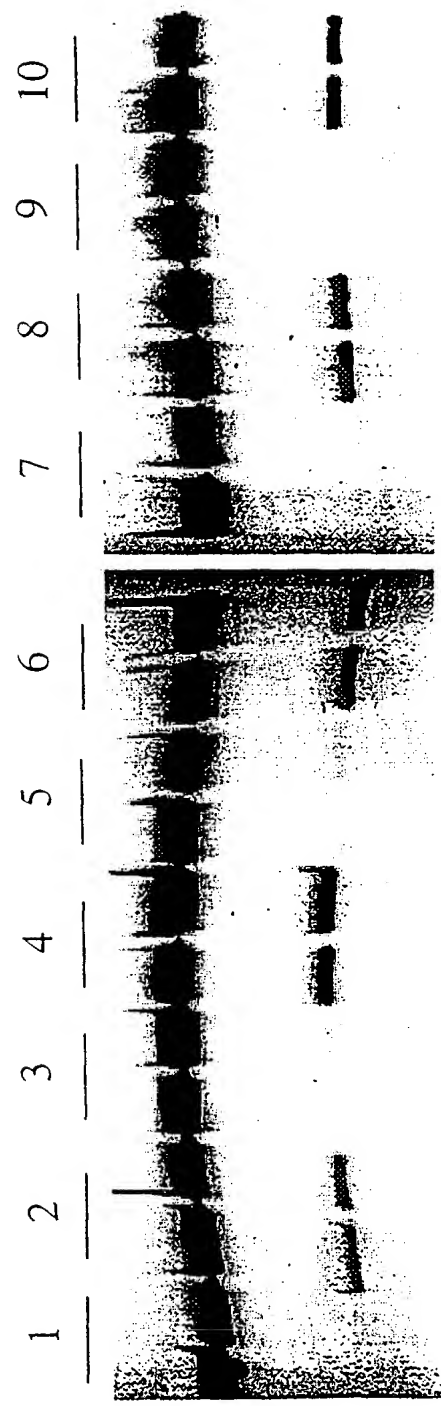
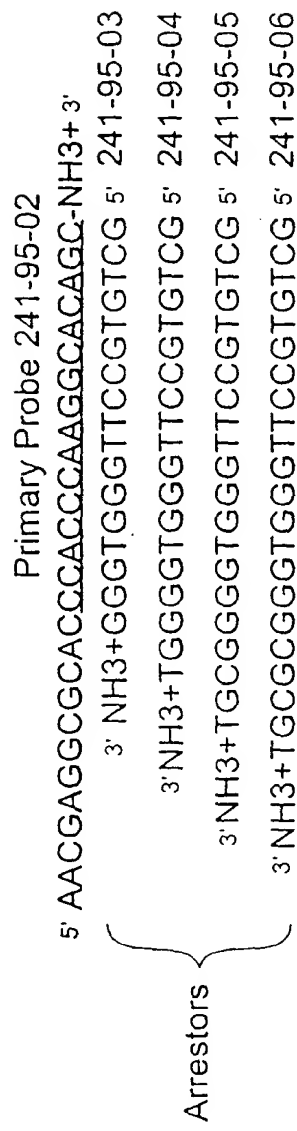


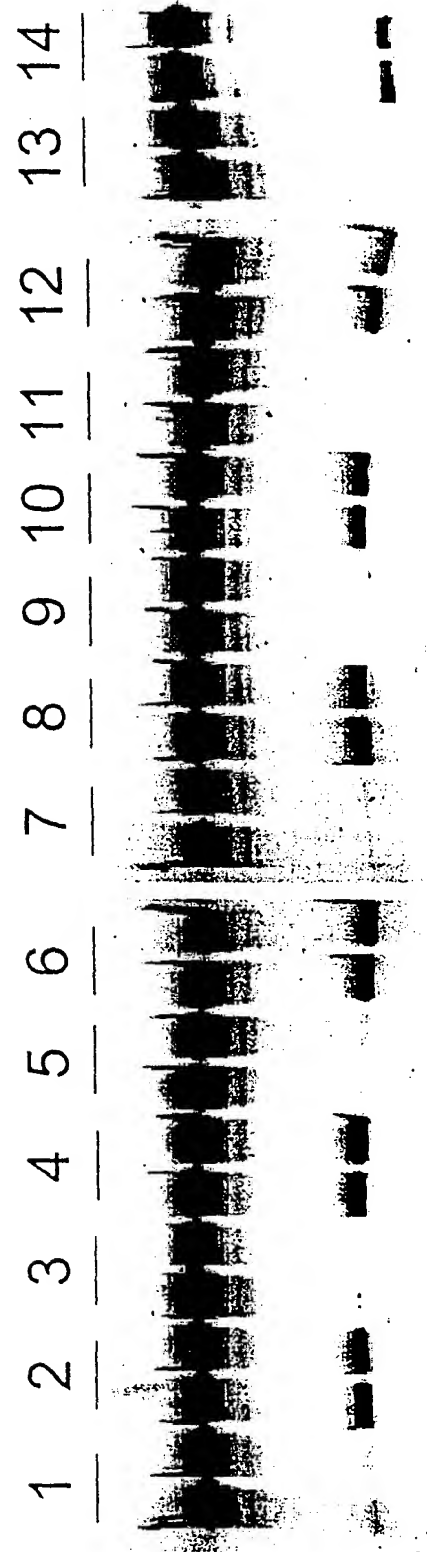
FIGURE 110C



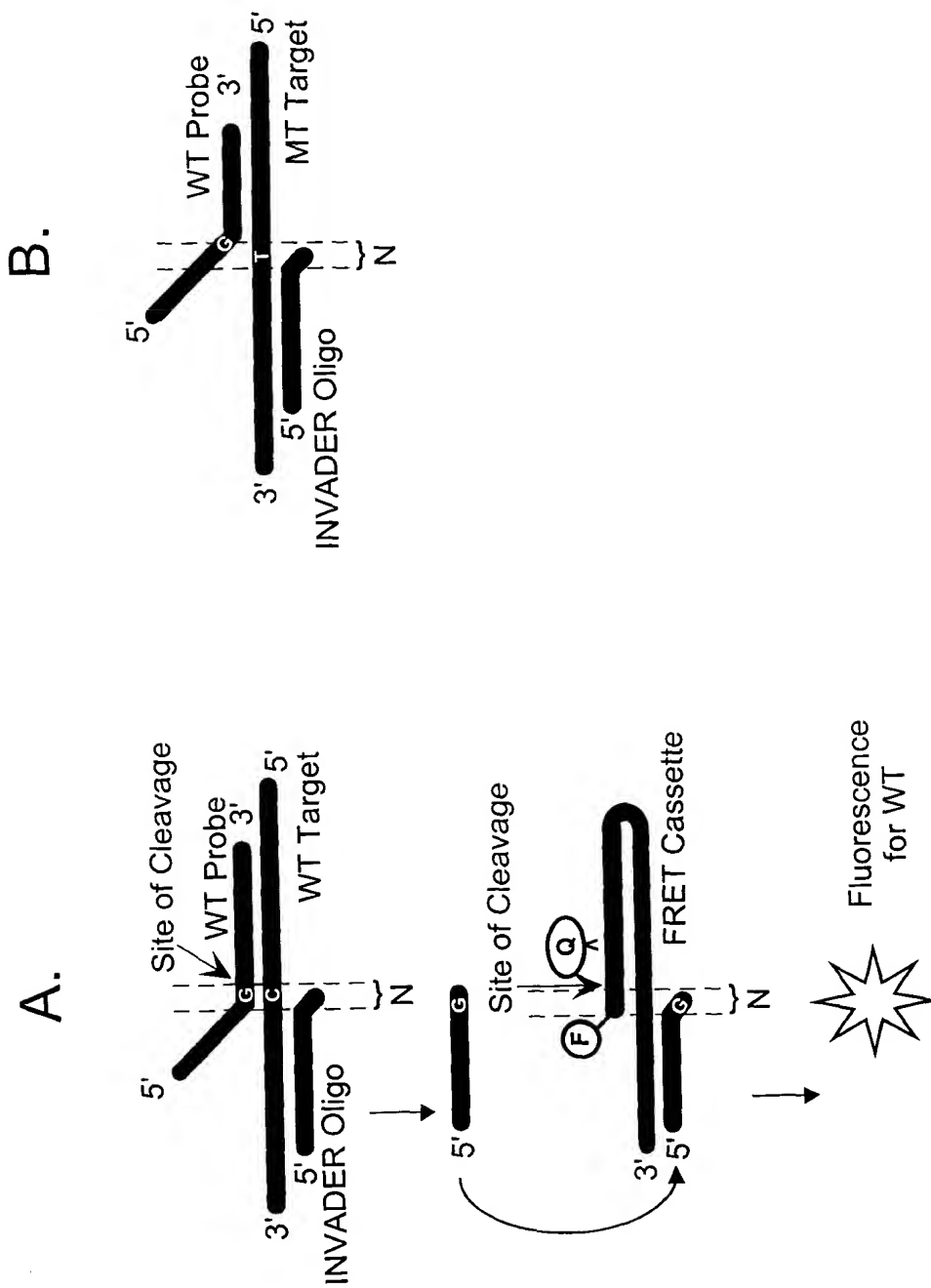
00577-703E1200

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FIGURE 111



# FIGURE 112



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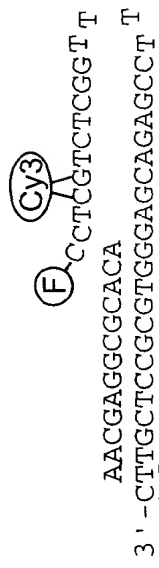
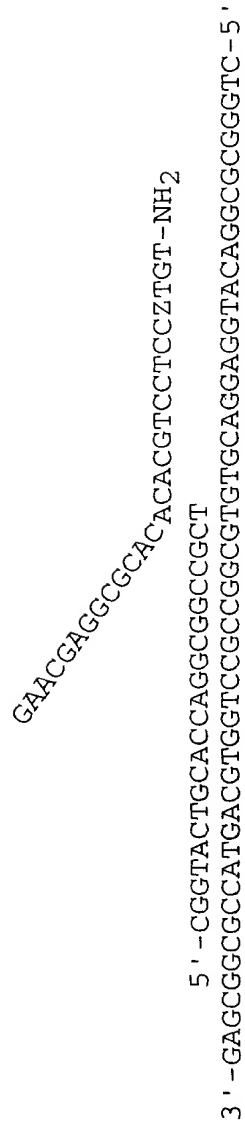
# FIGURE 113A

5'-AACGAGGCGCACGCACGTCTCCATGT  
5'-CGGTACTGCACCAAGGCGCGCGT  
3'-GAGCGCGCCATGACGTGTCGCGCGCGGTGCAGGAGGTACAGGCGCGGGTC-5'

(F) (Cy3) CCTCTCTCGGT  
AACGAGGCGCAG  
3'-CTTGCTCCGCGTGGGAGCAGAGCCCT

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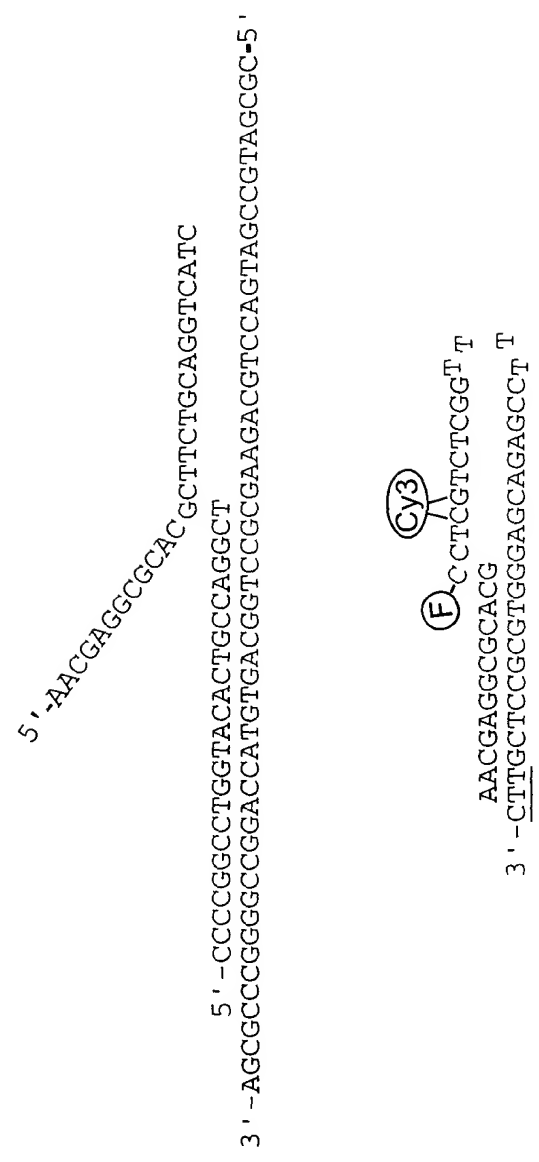
# FIGURE 113B





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# FIGURE 113C



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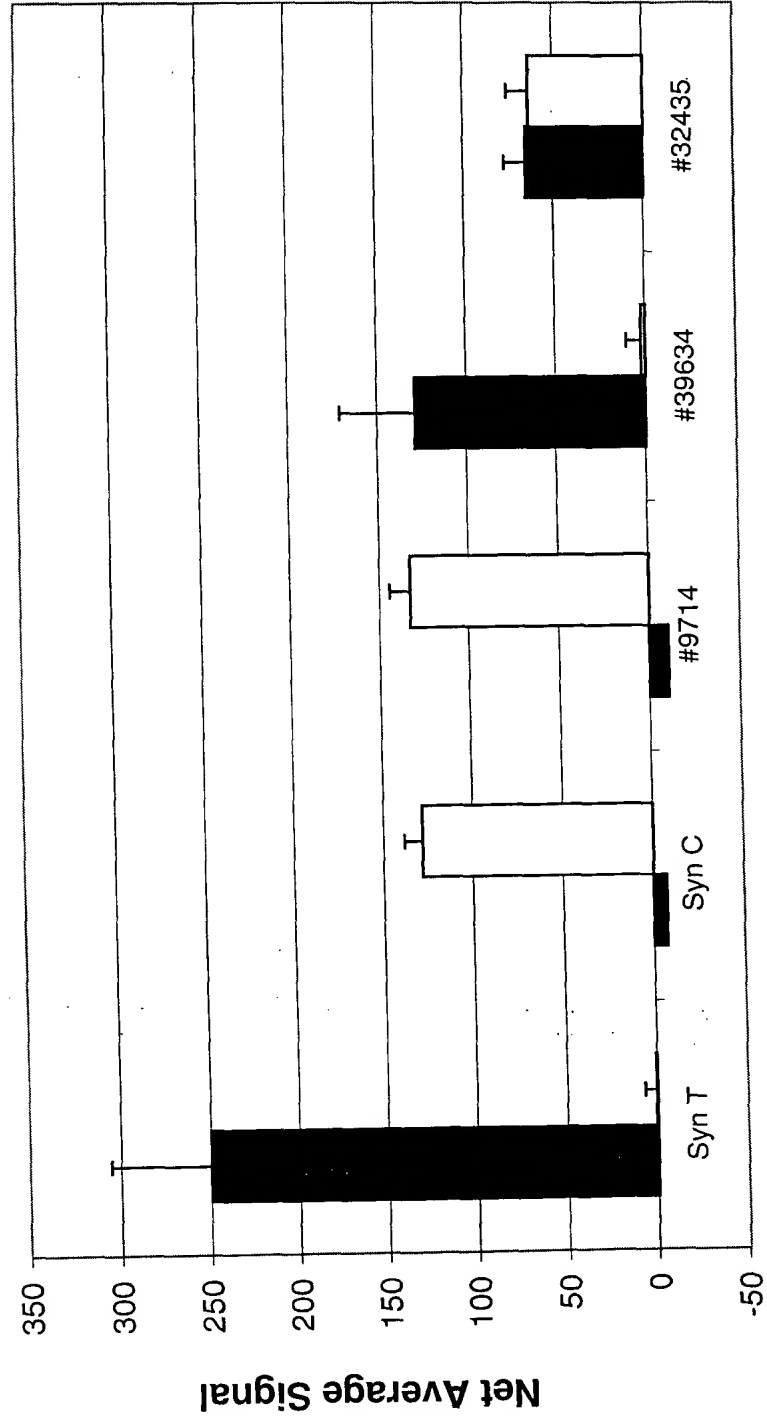
# FIGURE 113D

5' - AACGAGGCGCACACTTCTGCGZGGTCATC  
5' - CCCCCGGCCTGGTACACTGCCAGGCT  
3' - AGCGCCCGGGCCGGACCATGTGACGGTCCGTGAAGACGTCCAGTAGCCGTAGCGC - 5'

(F) C CTCGTCTCGGT T  
AACGAGGCGCACA  
3' - CTTGCTCCCGCGTGGGAGCAGAGCCCT T

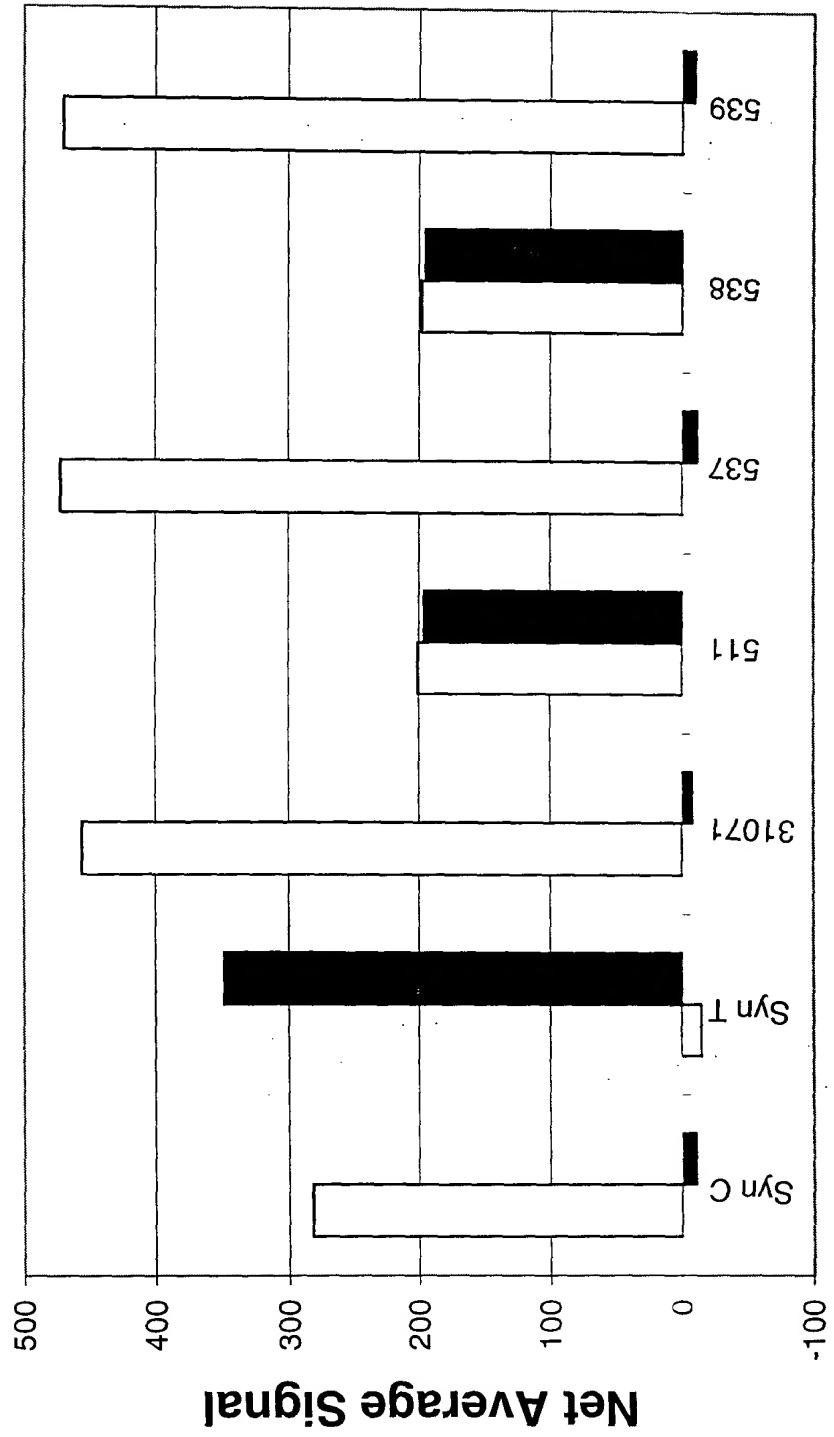
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FIGURE 114A



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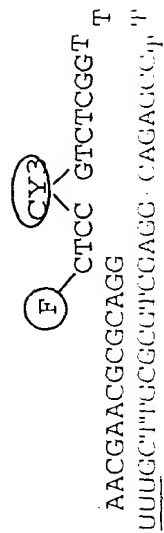
FIGURE 114B



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# FIGURE 115A

5'-AACGAACGGCAGGCCAGGTGGAGCATTT-3'  
5'-CCCCCTGGGGAAGACAGAGATATACGTC  
3'-GACCCCTTCTCGTCTCTATATGCACGGTCCACCTCGTGG-5'



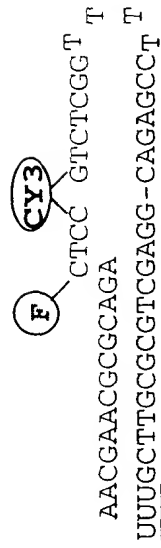
5' - A A C G A A C G C G C A G A C C A G G T G G A G C A C - 3'

## FIGURE 115B

5' - A A C G A A C G C G C A G A C C A G G T G G A G C A C - 3'

5' - C C C C T G G G A A G A G A G A G A T A T A C G T C

3' - G A C C C C T T C T C G T C T A T A T G C A T G G T C C A C C T C G T G G - 5'

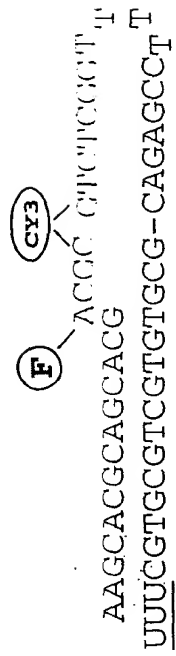


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# FIGURE 115C

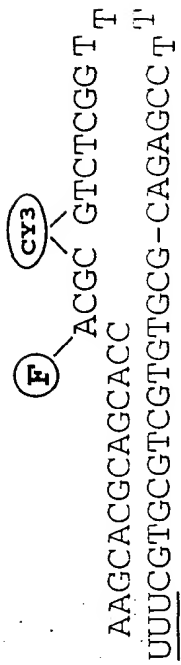
5'-AAGCAGCAGCAGCAGATCATAGAACACGAAACAGTTT-3'  
5'-GGGCTCCACACGGCGACTCTCATTT  
3'-GCCCGGAGGTGTGCCGCTGAGAGTACTAGTATCTTGTGCTTGTCGA-5'



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# FIGURE 115D

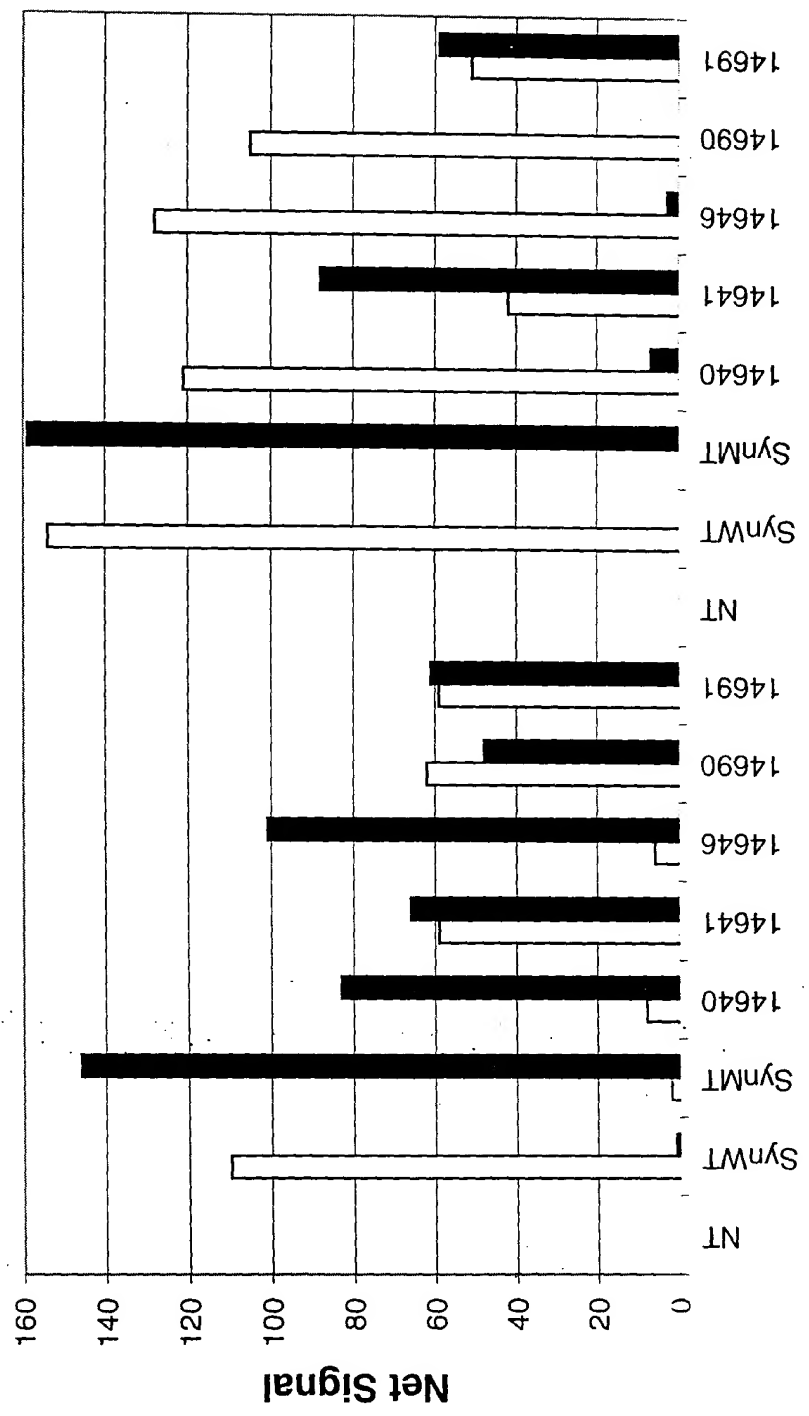
5'-AAGCAGCAGCACCATCATAGAACACGACGTTT-3'  
5'-GGGCTCCACACGGCGACTCTCATTT  
3'-GCCCCGAGGTGTGCCGCTGAGAGTAGTAGTATCTTGTGCTTGTCCGA-5'





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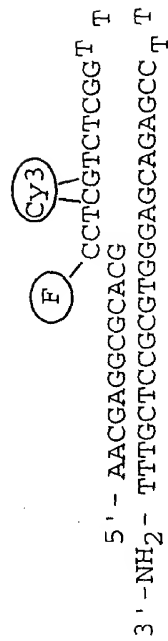
FIGURE 116



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# FIGURE 117A

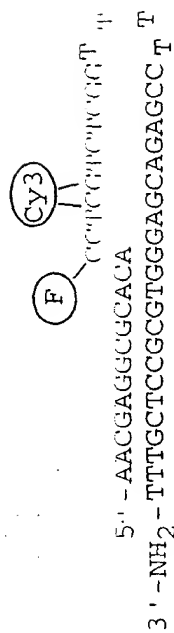
5'-AACGAGGCGCACGCTCCCGCAGACAC-3'  
5'-CAAAGAAAAGCTGCGTGATGATGAAATCGC  
3'-GGAGTTCTTTTCGACGCACTACTTtagccgagggcgctgtggaag-5'



sa/eth

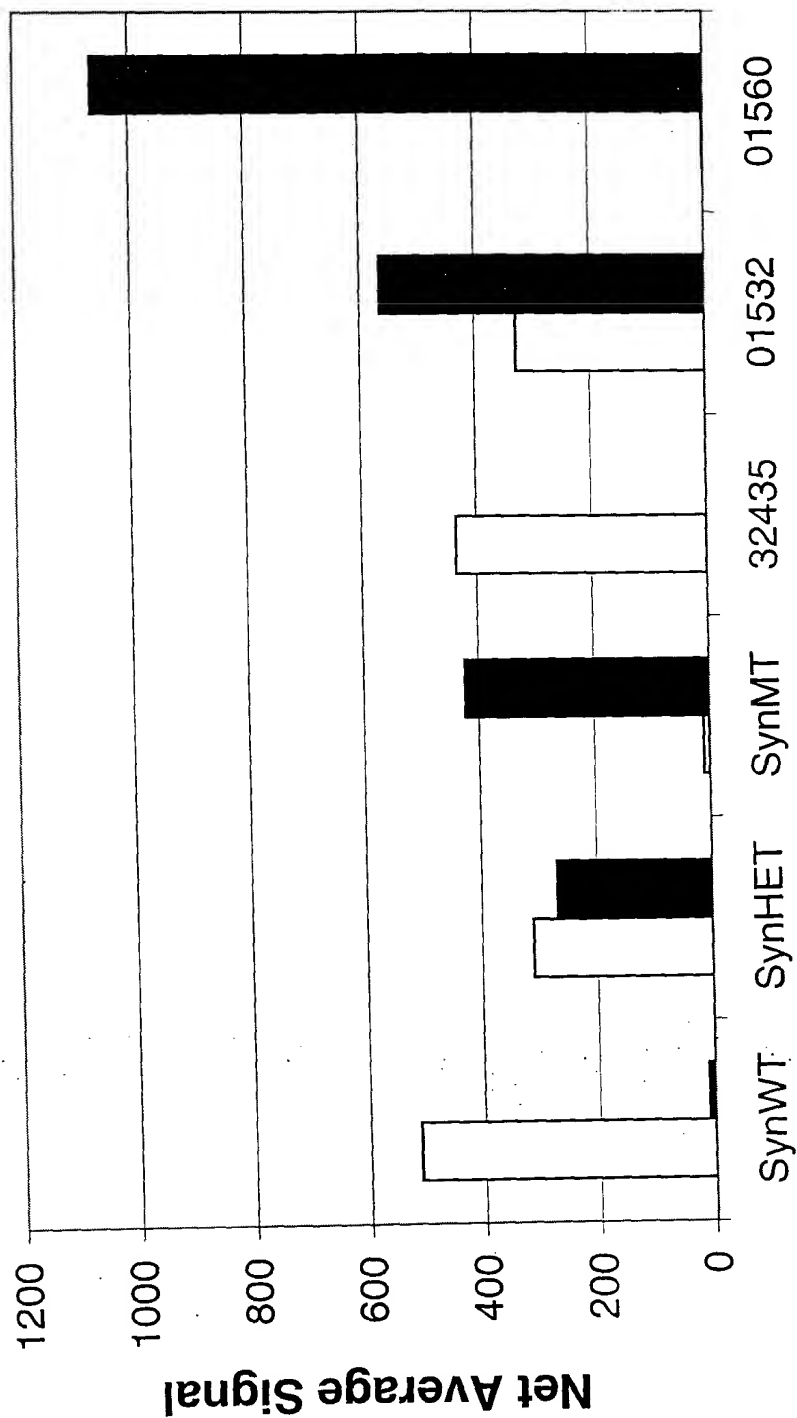
## FIGURE 117B

5'-AACGAGGCGCACTCCCGCAGACACC-3'  
5'-CAAAGAAAAGCTGCGTGATGATGAAATCGC  
3'-GGAGTTCTTTTCGACGCACTACTTCTAGCTGAGGGCGTCTGTGGAAG-5'



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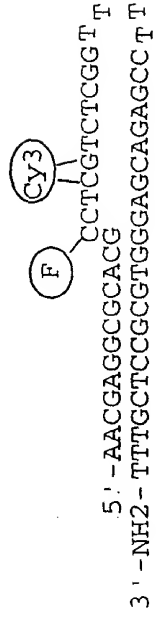
FIGURE 118



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# FIGURE 119A

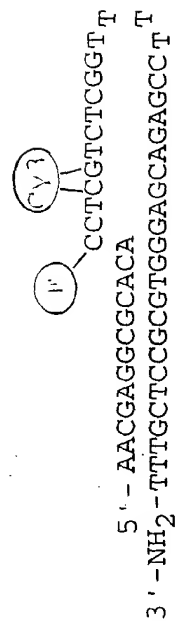
5'-AACGAGGCGCACGAGCCTCAATGCTCCC-NH2-3'  
5'-TATGGTTCCCAATAAAAGTGACTCTCAGCT  
3'-TTGATACCAAGGTTATTTTCACTGAGAGTCGCTCGGAGTTACGAGGGTCA-5'



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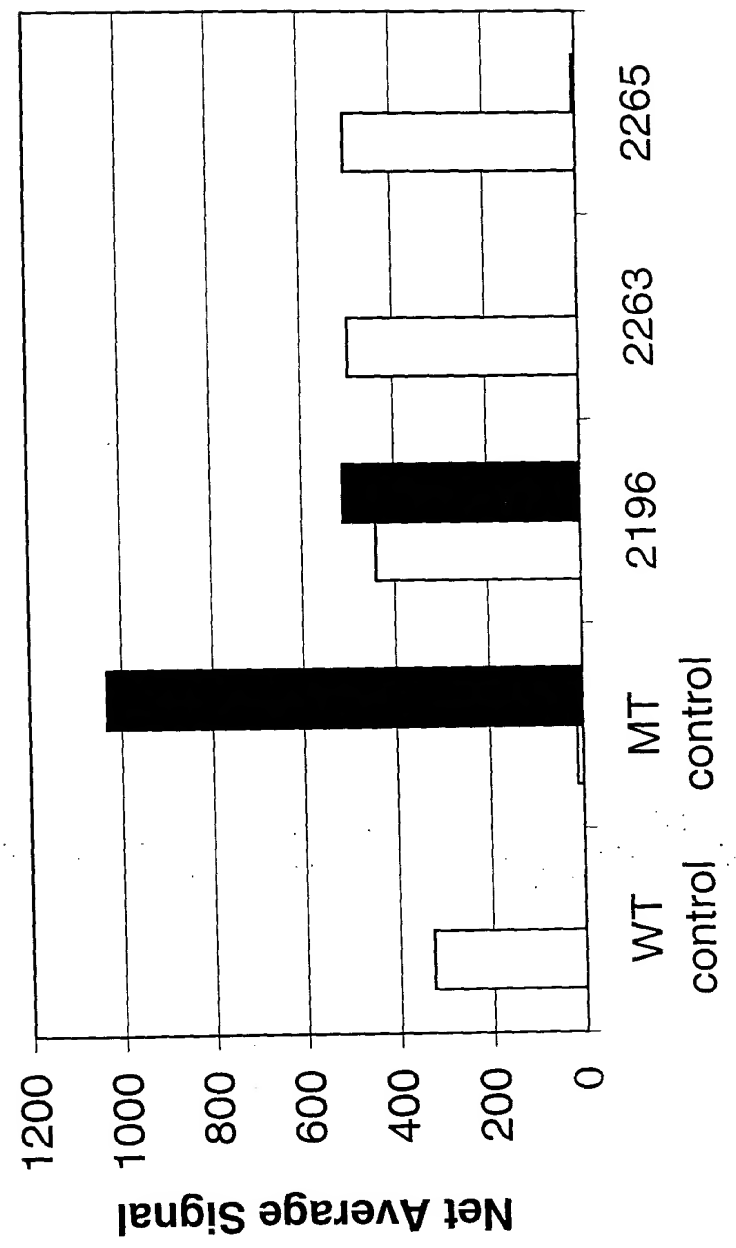
## FIGURE 119B

5'-AACGAGGCGCACAGCCTCAATGCTCCC-NH<sub>2</sub>-3'  
5'-TATGGTTCCCAATAAAAGTGACTCTCAGCT  
3'-TTGATACCAAGGGTTATTTTCACTGAGAGTCGTTCCGGAGTTACGAGGGTCA-5'



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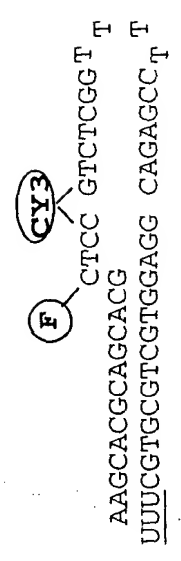
FIGURE 120



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# FIGURE 121A

5'-AAGCAGCGAGCAGC<sup>C</sup>GTACAACCCCTTTCTCTAGACAAA  
5'-AGATGCCCA<sup>T</sup>TTCTCCAGACCTCAGCCC  
3'-GTCTACGGGTAAAGAGGTCTGGAGTCGGCATGTTGGGAAAGAGATCTGAAGT-5'

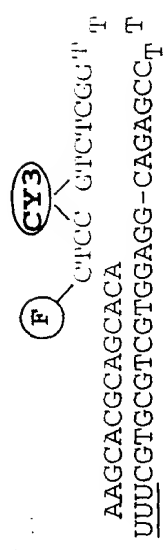




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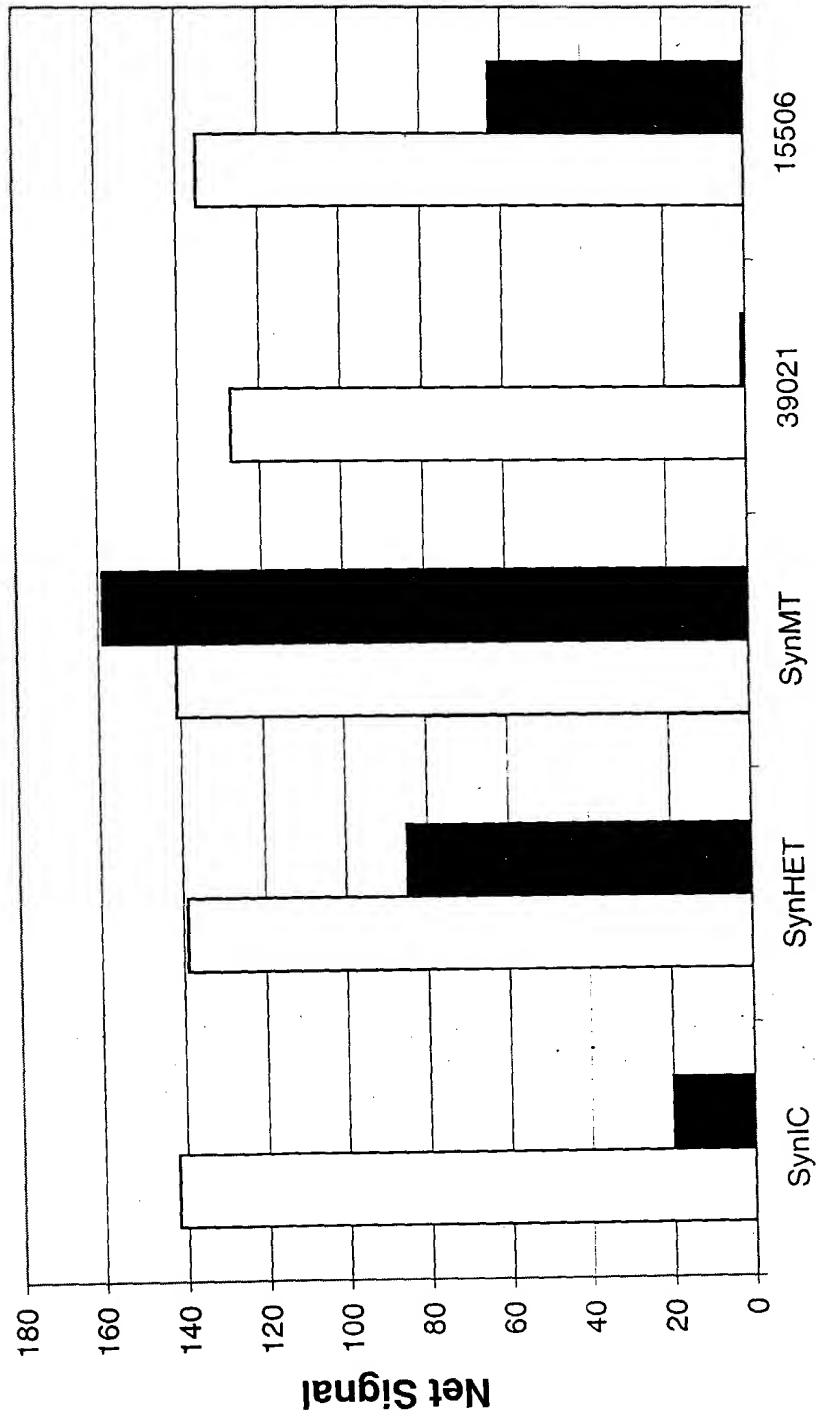
# FIGURE 121B

5'-AAGCAGGCAGCACAGGAACCCCTGTGACAT-3'  
5'-CCATCCAGGGAAGAGTGGCCGTGTT  
3'-GGTAGGTCCTTCTCACCGGACAATCCTTGGGACACTGTAAAGTTT-5'



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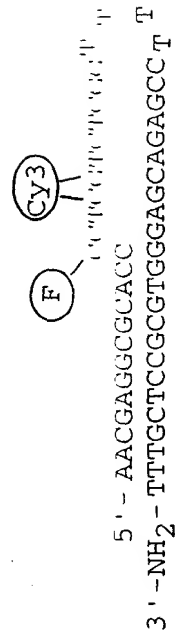
FIGURE 122



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# FIGURE 123A

5'-AACGAGGCGCACCCATGCCCCCTCAAAAC  
5'-GACCCCTGGAGGCTGAACCCCGTCCA  
3'-ATCCTGGGACCTCCGACTTGGGCAGGGGTACGGGGAGTTTGGAT-5'

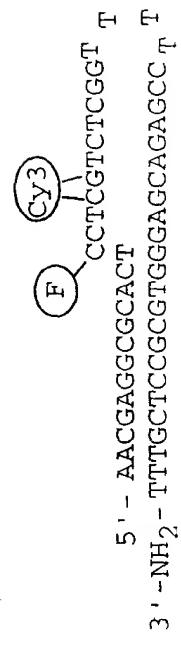


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5'-AACGAGGCGCAC TCATGCCCCCTCAAAAC

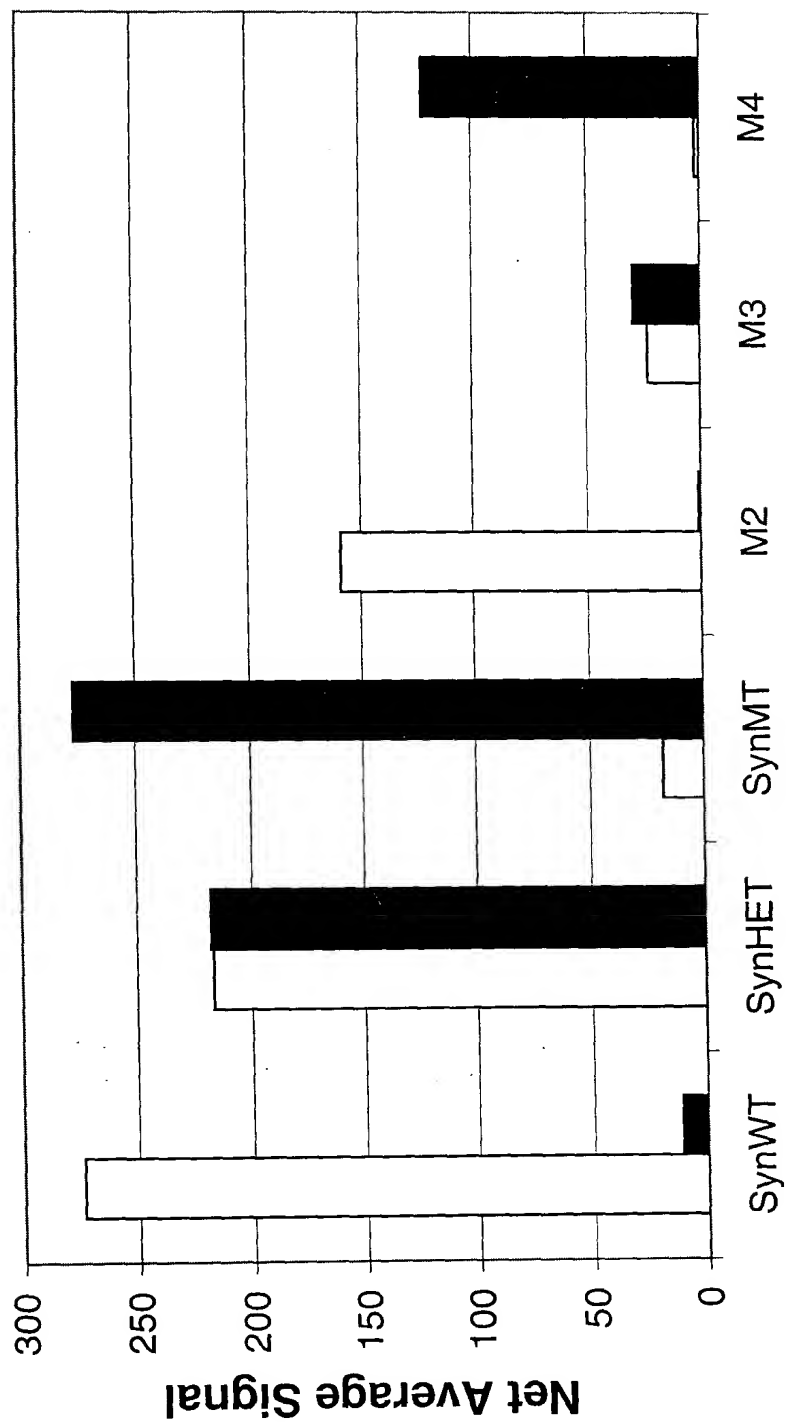
# FIGURE 123B

5'-AACGAGGCGCAC TCATGCCCCCTCAAAAC  
5'- GACCCCTGGAGGCTGAACCCCGTCCA  
3'- ATCCTGGGACCTCCGACTTGGGGCAGGAGTACGGGGAGTTTGGGAT-5'



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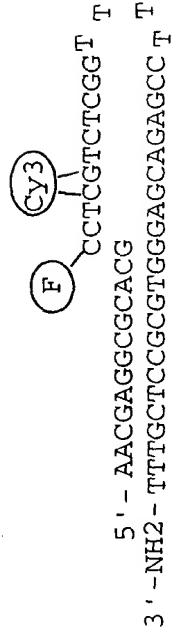
FIGURE 124



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# FIGURE 125A

5' - AACGAGGCGCAC GAGGAATACAGGTATTTTGTGTC-NH3  
5' - TAATCTGTAAGAGCAGATCCCTGGACAGGCC  
3' - AGATTAGACATTCTCGTCTAGGGACCTGTCCGCTCCTTATGTCCATATAAACAGGAA-5'



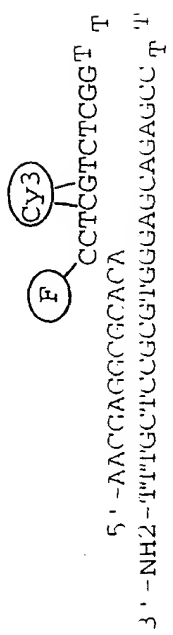
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# FIGURE 125B

AACGAGGCGCAC AAGGAAATACAGGTATTTGTC-NH3

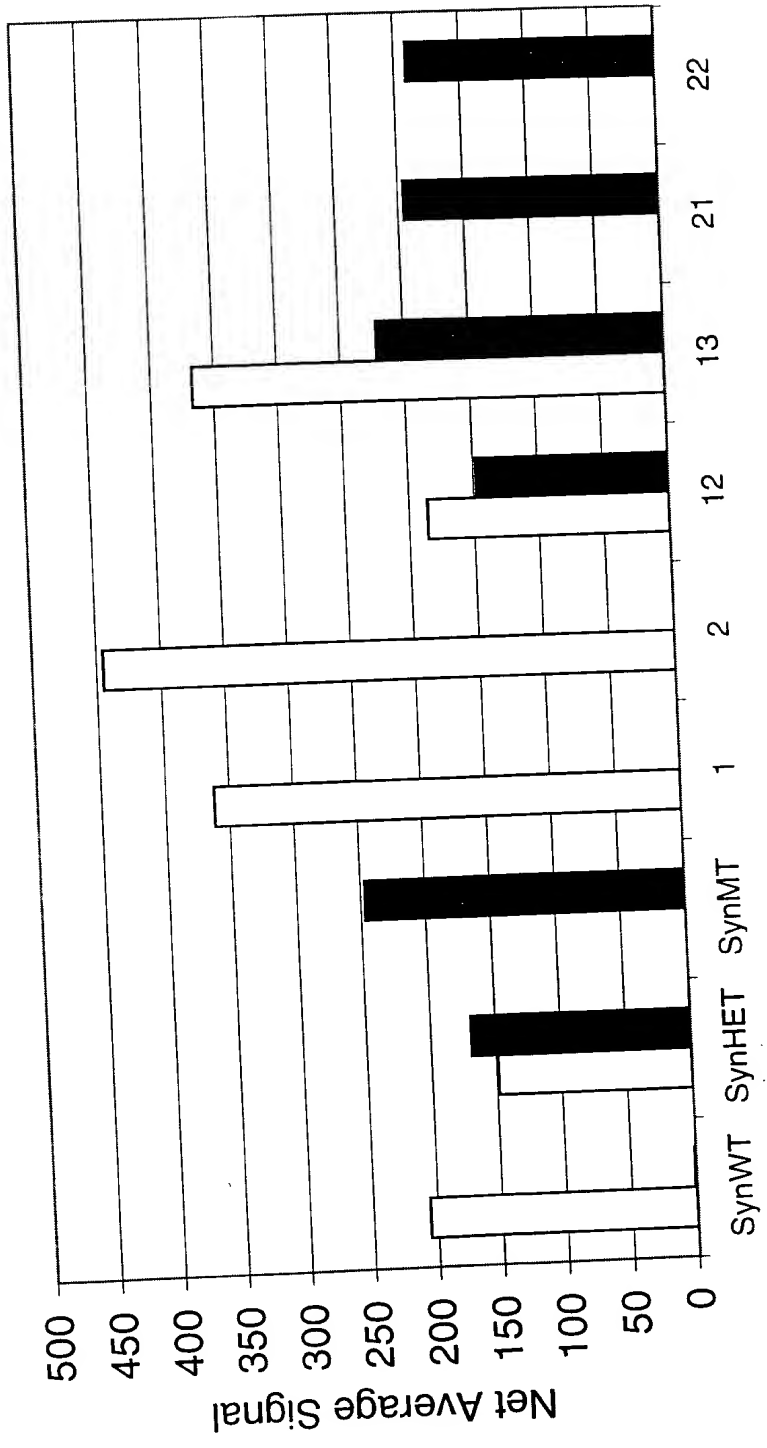
5' - TAATCTGTAAGAGCAGATCCCTGGACAGGCC

3' - AGATTGACATTCGTCCTAGGGACCTGTCCGTTCCCTTATGTCCATAAAACAGGAA - 5'



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FIGURE 126





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## FIGURE 127A

5' - GCGCCGAGG TCTTGGGGTGGTTACAAG - NH<sub>2</sub> - 3'   
 5' - GGTAAGGTTGGCAAAAAGATAAC   
 CCATTCCAACCGTTTTTCTATTAGAACCCCAATGTTTC - 5'

(F) (CY3) TCTC GTCTCGGT T   
 5' - GCGCCGAGGT   
 B - GCGCGGCTCCAGAGTCAGAGCC T

5' - CACTTGCTTCAGGACCATATTTCCTCTC

## FIGURE 127B

5' - CACTTGCTTCAGGACCATATTTCCTCTC  
GTGAACGAAAGTCCTGGTATAAAGAGAGATGTGGAATAATCCACGAAACA - 5'

5' - CCGCGCCGAGGACACCTTTTTTAGGGTGCTTTGT - NH<sub>2</sub> - 3'  
GTGAACGAAAGTCCTGGTATAAAGAGAGATGTGGAATAATCCACGAAACA - 5'

CY3

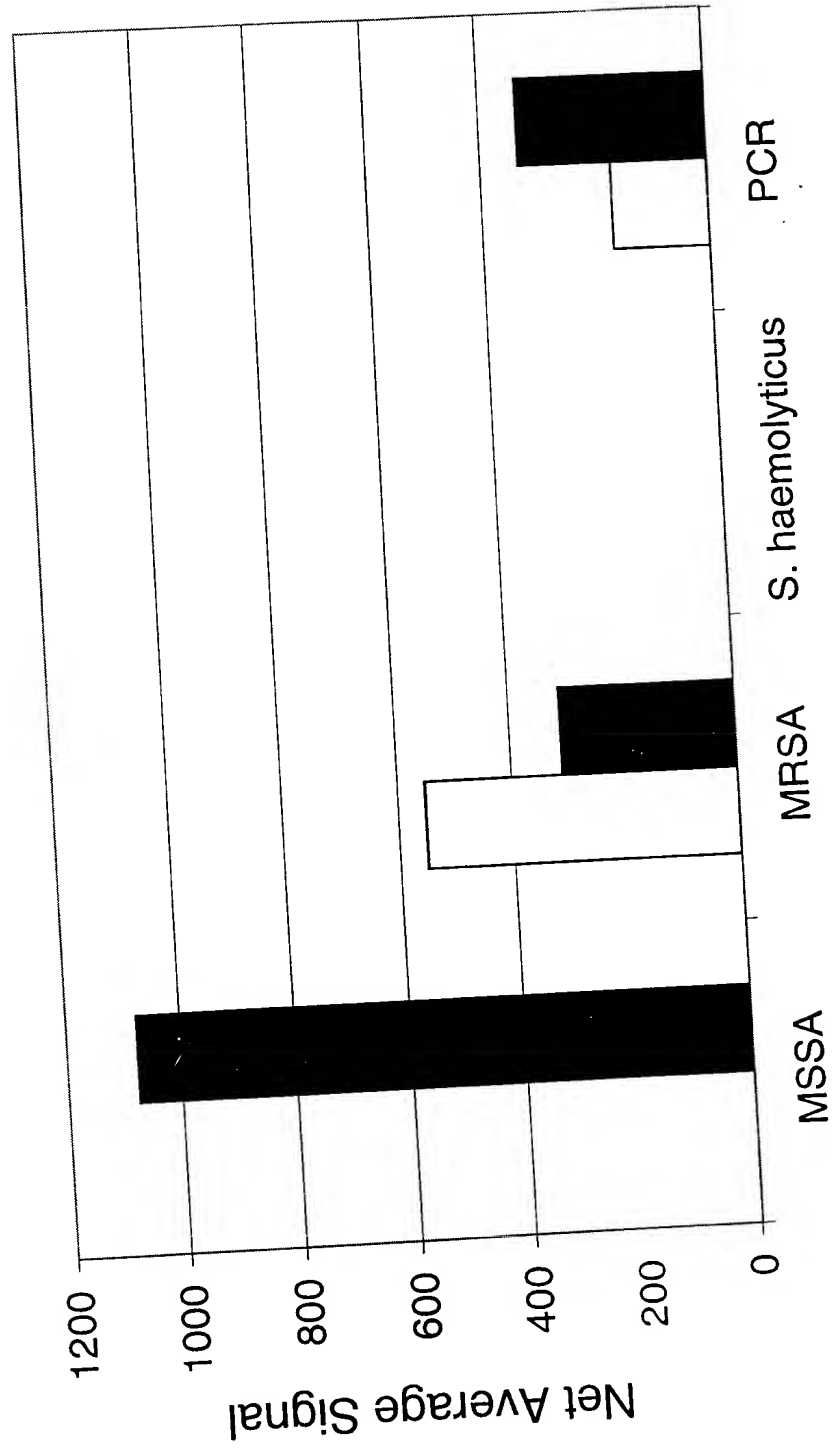
F

5' - CCGCGCCGAGGACACCTTTTTTAGGGTGCTTTGT - NH<sub>2</sub> - 3'  
GTGAACGAAAGTCCTGGTATAAAGAGAGATGTGGAATAATCCACGAAACA - 5'

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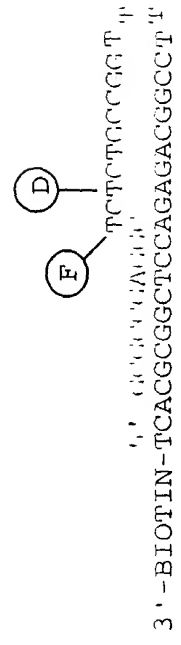
FIGURE 128



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# FIGURE 129

5' GCGCCGAGG CCGTTCTCTAGCGTGA-PO4 3'  
5' CCGAAGCACGCACAAAGCGGTGTGTACGA  
3' GGCTTCGTGCGTGTTCGCCACCCAGTGGCGGCAAGAGATCGCCACTGCGGACATATG 5'



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FIGURE 130

